



## SEQUENCE LISTING

- <110> Pompejus, Markus  
Kroger, Burkhard  
Schroder, Hartwig  
Zelder, Oskar  
Haberhauer, Gregor
- <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
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 Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu  
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 Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu  
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 Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala  
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 Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu  
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 Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala  
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&lt;223&gt; RXA00204

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Met Val Asn Ser Glu
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caa gcg ctt cat cag cat gat cct gca cca atc ctt cag ttg gat aaa 163
Gln Ala Leu His Gln His Asp Pro Ala Pro Ile Leu Gln Leu Asp Lys
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Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu Gly Glu Asn Gly Ala
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Lys Leu Arg Gly Gly Asp Ile Ser Glu Ala Ile Lys Asn Gly Ile Gly	
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His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu Val Leu Gly Ser Ser	
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<213> Corynebacterium glutamicum

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Gln	Pro	Ile	Ser	Asp	Leu	Ser	Gly	Gly	Asn	Gln	Gln	Lys	Ala	Val	Phe
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Gly	Arg	Trp	Val	Leu	Ala	Gly	Ser	Asn	Val	Leu	Leu	Leu	Asp	Glu	Pro
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Gly	Arg	Ile	Ala	Gly	Glu	Leu	Pro	Ala	Lys	Gly	Thr	Thr	Gln	Asp	Asp
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caa ctc cgc gaa gta tcc aaa aaa tac ggt gct ttc cag gcc ctc aac 163  
Gln Leu Arg Glu Val Ser Lys Lys Tyr Gly Ala Phe Gln Ala Leu Asn  
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gac aac ggc gcc gga aaa tcc acc ctc atc aag att ctc tcc ggc ctg 259  
Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Ile Leu Ser Gly Leu  
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His Pro Ala Thr Ser Gly Glu Val Ile Val Ala Gly Asp Val Val Asn  
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Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser Gly Gly Gln Arg Gln  
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Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly Ala Arg Val Leu Ile  
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<213> Corynebacterium glutamicum

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Thr Cys Val Leu Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys  
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Ile Leu Ser Gly Leu His Pro Ala Thr Ser Gly Glu Val Ile Val Ala  
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Gly Asp Val Val Asn Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly  
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Ile Ala Thr Val Tyr Gln Asp Leu Ala Val Val Gly Gln Met Ser Val  
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Gln Ser Gly Met Val Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly  
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<213> Corynebacterium glutamicum

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 85 90 95  
 Gly Ala Ile Ser Gly Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe  
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 145 150 155 160  
 Ala Gly Ile Val Cys Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg  
 165 170 175  
 Ser Met Tyr Ala Ile Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly  
 180 185 190  
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 195 200 205  
 Tyr Ala Ala Leu Ala Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala  
 210 215 220  
 Gln Pro Gln Ala Gly Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val  
 225 230 235 240  
 Val Ile Gly Gly Ala Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly  
 245 250 255  
 Thr Leu Ile Gly Ala Ile Leu Leu Ala Val Ile Arg Asn Gly Leu Asn  
 260 265 270  
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Glu Phe Gly Leu Leu Tyr Gly Val Val Ala Leu Gly Val Tyr Leu Thr
                        10 15 20

ttc cgt gtg ctc aac ttt ccc gac ctc acc gtt gac ggc agc ctg acc 211
Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val Asp Gly Ser Leu Thr
                        25 30 35

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Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met Ser Gly Trp Pro Pro
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ctt atg gct act gcc gct ggt ttc gtt act ggc ttt atc gct ggc atg 307
Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly Phe Ile Ala Gly Met
                        55 60 65

atc acc ggt ttg ctg cac acc aag ggc aag atc gat ggt ttg ctc gca 355
Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile Asp Gly Leu Leu Ala
                        70 75 80 85

ggt att ttg acc atg att gcg ttg tgg tcg gtt aac ttg cgc atc atg 403
Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val Asn Leu Arg Ile Met
                        90 95 100

ggt ggc gcg aac gtg cca ttg ttg cgc acc gat aac ctc ttc acc ccg 451
Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp Asn Leu Phe Thr Pro
                        105 110 115

ctt cgc gac gcc ggc ctc ctc ggc aca tgg gca ggc ccg gcg atc ctc 499
Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala Gly Pro Ala Ile Leu
                        120 125 130

gcc gtt gca gtg gga att ttg gga ctc atc gtc atc tgg ttc ctc aac 547
Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val Ile Trp Phe Leu Asn
                        135 140 145

act gat atc gga ctg tcg ctg cga tcc acc ggc gac aac ggg ccg atg 595
Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly Asp Asn Gly Pro Met
                        150 155 160 165

gtg cag tcc ttt ggt gtt tca acg gat ttc acc aaa atc ctc acc atc 643
Val Gln Ser Phe Gly Val Ser Thr Asp Phe Thr Lys Ile Leu Thr Ile
                        170 175 180

tcc ctg tcc aat ggt ttt gtt ggt ctt gcc ggt gca ctc atc gct cag 691
Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly Ala Leu Ile Ala Gln
                        185 190 195

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tac cag ggc ttc gca gat att tcg atg ggt att ggc ctc atc gtg atc 739  
 Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile Gly Leu Ile Val Ile  
 200 205 210  
 ggt ctc gca tcg gtt att ttg ggc cag gcc atc ttc ggt cag cgt cgc 787  
 Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile Phe Gly Gln Arg Arg  
 215 220 225  
 gtg tgg ttg gct gtg ttg gct gtc atc gtc ggt gcc atc gcg tac cgc 835  
 Val Trp Leu Ala Val Leu Ala Val Ile Val Gly Ala Ile Ala Tyr Arg  
 230 235 240 245  
 ctg atc att ttc gca gca ctg cgc gtt ggc ctt gac ccc aac gat atg 883  
 Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu Asp Pro Asn Asp Met  
 250 255 260  
 aag gca att tct gcg atc ttg gtg gtt gtc gcc atg ctg ctg ccg agg 931  
 Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala Met Leu Leu Pro Arg  
 265 270 275  
 tgg cgt gcg aag ttc tcc aag gca ccg aag cct aag caa cca gta gca 979  
 Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro Lys Gln Pro Val Ala  
 280 285 290  
 gtg gag gct taagacatgt tatccatcaa cgg 1011  
 Val Glu Ala  
 295

<210> 16  
 <211> 296  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 16  
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 Gly Val Tyr Leu Thr Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val  
 20 25 30  
 Asp Gly Ser Leu Thr Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met  
 35 40 45  
 Ser Gly Trp Pro Pro Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly  
 50 55 60  
 Phe Ile Ala Gly Met Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile  
 65 70 75 80  
 Asp Gly Leu Leu Ala Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val  
 85 90 95  
 Asn Leu Arg Ile Met Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp  
 100 105 110  
 Asn Leu Phe Thr Pro Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala  
 115 120 125  
 Gly Pro Ala Ile Leu Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val

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<210> 17
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1123)
<223> RXA02439
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acgttgatgt cattgctgaa gccgttgggg agggctctgcg atg aca aaa atc aag 115
Met Thr Lys Ile Lys
1 5
agt ggg gag gcg tcg aca agc att gtt gag cgc gcc tta aag cgc ccc 163
Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg Ala Leu Lys Arg Pro
10 15 20
gaa ctg acc agc ctg ctt ggc gcc gtg ctt gtt ttt acg ctg ttt atg 211
Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val Phe Thr Leu Phe Met
25 30 35
gtg gtc gcg ccg gca ttt agg tca tgg gat tcg atg gcg acc gtg ctg 259
Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser Met Ala Thr Val Leu
40 45 50

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tat gcg agt tcc acg atc ggc atc atg gcg gtt gcc gtg ggc ctg ctg	307
Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val Ala Val Gly Leu Leu	
55 60 65	
atg atc gct gat gaa ttc gac ctg tcc acc ggc gtt gcc gtg aca act	355
Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly Val Ala Val Thr Thr	
70 75 80 85	
gca gcg ctg gcg gcc tcg atg ttt agc tat aac ctg tgg ctg aac acc	403
Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn Leu Trp Leu Asn Thr	
90 95 100	
tgg gtg ggc gcg ctg att gca ttg gtg att tcg ctg gcc atc ggc ttt	451
Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser Leu Ala Ile Gly Phe	
105 110 115	
ttc aac ggc ttt ttg gta gtg aaa acc aag att gca tcc ttc ctg atc	499
Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile Ala Ser Phe Leu Ile	
120 125 130	
acc ctt gcc act ttc ctt atg ctg cag ggt att aat ctg gcg gtc acc	547
Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile Asn Leu Ala Val Thr	
135 140 145	
aag ctg att tcc ggc acc gtg gcc acg cca acc atc gcg gat atg gaa	595
Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr Ile Ala Asp Met Glu	
150 155 160 165	
ggt ttt cct tca gcg cgt gcg gtg ttt gcc agc tcg att ccc atc ttt	643
Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser Ser Ile Pro Ile Phe	
170 175 180	
ggt gtg aat att cgc atc act gtt ttt tgg tgg ctg ctg ttt gtt atc	691
Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp Leu Leu Phe Val Ile	
185 190 195	
gtc ggc act ttt gtg ttg ttt aag acg cgc atc ggc aac tgg att ttt	739
Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile Gly Asn Trp Ile Phe	
200 205 210	
gcg gtc ggt ggc gat gaa gag gca gct cgc gca gtc ggc gtt ccc gtg	787
Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala Val Gly Val Pro Val	
215 220 225	
cgt ggc gtg aaa atc ggc ctg ttc atg ttc gtt ggt ttt gcc gcc tgg	835
Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val Gly Phe Ala Ala Trp	
230 235 240 245	
ttt gtg ggc atg cac aac ctg ttc ctc ttt gat tcg att cag gct ggt	883
Phe Val Gly Met His Asn Leu Phe Leu Phe Asp Ser Ile Gln Ala Gly	
250 255 260	
caa ggc gtg ggt aat gag ttc ctc tac atc atc gct gcg gtg atc gga	931
Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile Ala Ala Val Ile Gly	
265 270 275	
ggc atc tcc atg act ggt ggc cgc gga aca gtg gtg ggc aca atg att	979
Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val Val Gly Thr Met Ile	
280 285 290	

ggt gca ctc atc ttt gga atg acc aac caa ggc att gtt tat gca ggt 1027  
 Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly Ile Val Tyr Ala Gly  
 295 300 305

tgg aac cct gac tgg ttc atg ttc ttc ctc ggc ggc acc cta ctt ctg 1075  
 Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly Gly Thr Leu Leu Leu  
 310 315 320 325

gct gtt ttg ctc aat cac cga ttc gag cgt ttc aac aag gag cga tca 1123  
 Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe Asn Lys Glu Arg Ser  
 330 335 340

tgacagacct cattcaactc cgc 1146

<210> 18

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

Met Thr Lys Ile Lys Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg  
 1 5 10 15

Ala Leu Lys Arg Pro Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val  
 20 25 30

Phe Thr Leu Phe Met Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser  
 35 40 45

Met Ala Thr Val Leu Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val  
 50 55 60

Ala Val Gly Leu Leu Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly  
 65 70 75 80

Val Ala Val Thr Thr Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn  
 85 90 95

Leu Trp Leu Asn Thr Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser  
 100 105 110

Leu Ala Ile Gly Phe Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile  
 115 120 125

Ala Ser Phe Leu Ile Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile  
 130 135 140

Asn Leu Ala Val Thr Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr  
 145 150 155 160

Ile Ala Asp Met Glu Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser  
 165 170 175

Ser Ile Pro Ile Phe Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp  
 180 185 190

Leu Leu Phe Val Ile Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile  
 195 200 205

Gly Asn Trp Ile Phe Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala

210                      215                      220  
 Val Gly Val Pro Val Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val  
 225                      230                      235                      240  
 Gly Phe Ala Ala Trp Phe Val Gly Met His Asn Leu Phe Leu Phe Asp  
                     245                      250                      255  
 Ser Ile Gln Ala Gly Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile  
                     260                      265                      270  
 Ala Ala Val Ile Gly Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val  
                     275                      280                      285  
 Val Gly Thr Met Ile Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly  
                     290                      295                      300  
 Ile Val Tyr Ala Gly Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly  
 305                      310                      315                      320  
 Gly Thr Leu Leu Leu Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe  
                     325                      330                      335  
 Asn Lys Glu Arg Ser  
                     340

<210> 19  
 <211> 746  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(723)  
 <223> RXN02994

<400> 19  
 atc aag atg acg gga gtg caa aaa tac ttc ggc gac ttt cat gcc ctt    48  
 Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu  
   1                      5                      10                      15  
 acg gat att gat ctt gaa att ccc aga gga caa gtt gtc gtc gta ctt    96  
 Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu  
                     20                      25                      30  
 gga cca tcc gga tcc ggc aag tca acc ctt tgc cgc acg atc aac cgt    144  
 Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg  
                     35                      40                      45  
 ctc gaa acc atc gag gaa ggc acc atc gaa atc gat gga aag gtt ctc    192  
 Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu  
                     50                      55                      60  
 cca gaa gaa ggt aaa ggc tta gcc aat ctc cgc gcc gat gtc gga atg    240  
 Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met  
   65                      70                      75                      80  
 gta ttc cag tcc ttc aac ctc ttc ccc cac ctc acc atc aaa gac aac    288  
 Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn  
                     85                      90                      95

gtc act ctt gca ccc atc aaa gtg cga aag atg aaa aag tct gaa gcc 336  
 Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala  
 100 105 110

gaa aag ctt gcg atg agc ctg ttg gaa cgc gtc ggc atc gca aac caa 384  
 Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln  
 115 120 125

gct gat aaa tat ccg gcg caa ctg tcc ggc ggt cag caa cag cgt gtg 432  
 Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val  
 130 135 140

gcc atc gcg cgc gca ctt gcg atg aac cca aag atc atg ctt ttc gac 480  
 Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp  
 145 150 155 160

gag ccc acc tcc gcc ctt gac cct gaa atg gtc aac gaa gtg ttg gac 528  
 Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp  
 165 170 175

gtc atg gca agc ctt gcc aag gaa ggc atg acg atg gtg tgt gtt acc 576  
 Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr  
 180 185 190

cac gag atg gga ttc gca cgc aaa gca gcc gat cgt gtg ttg ttc atg 624  
 His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met  
 195 200 205

gcg gat ggg ctc att gtg gaa gat acg gaa cca gat tcc ttc ttc acc 672  
 Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr  
 210 215 220

aac cct aag tct gat cgt gca aaa gac ttc ctc ggc aag atc ctt gcc 720  
 Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala  
 225 230 235 240

cac tagtttttgg ctgcgcctct atc 746  
 His

<210> 20  
 <211> 241  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 20  
 Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu  
 1 5 10 15

Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu  
 20 25 30

Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg  
 35 40 45

Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu  
 50 55 60

Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met

65	70	75	80
Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn	85	90	95
Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala	100	105	110
Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln	115	120	125
Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val	130	135	140
Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp	145	150	155
Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp	165	170	175
Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr	180	185	190
His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met	195	200	205
Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr	210	215	220
Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala	225	230	235
His			

<210> 21  
 <211> 1790  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1767)  
 <223> FRXA01245

<400> 21	
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Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe	
1 5 10 15	
tgg tgg gaa ctg gcc ctg ctg gtg acc ata atg ctg ttg ggc cac tgg	96
Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp	
20 25 30	
ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg ctg	144
Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu	
35 40 45	
gca gcg ctc ctg ccc gat gag gcc gag aag gtc gtc gac ggg acc acc	192
Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr	



50	55	60	
cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg gtc			240
Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val			
65	70	75	80
cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atg gac gga gcg			288
Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala			
	85	90	95
gcc gaa ttc gat gag gcc atg atc acc ggc gaa tcc cga ccc gtc tac			336
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr			
	100	105	110
cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac aac			384
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn			
	115	120	125
acc gtc cgt atc cgg gtg gag gcc acc ggt ggg gac acc gcc ctg gca			432
Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala			
	130	135	140
ggc atc cag cgc atg gtc gcc gac gcc cag gcc tcc tcc tcc cgg gcc			480
Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala			
	145	150	155
cag gcc ctg gcc gat cga gcc gca gcc tta ctg ttc tgg ttc gcc ctg			528
Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu			
	165	170	175
atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc ccc			576
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro			
	180	185	190
gac gat gcc gtg gtc cgc gcg gtg acc gtg ctg atc atc gcc tgc ccg			624
Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro			
	195	200	205
cac gcc ctg ggc ctg gcc atc ccg ctg gtc atc gcg atc tcc tcc gag			672
His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu			
	210	215	220
cgc gcc gcg aaa tcc ggg gtg ctc atc aag gac cgc atg gca ctc gag			720
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu			
	225	230	235
cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc ctg			768
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu			
	245	250	255
acc gaa ggc gca cac gcc gtc acc ggc gtg gct ccg gcc acg ggt atc			816
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile			
	260	265	270
gcc gag ggt gag ctg ctg gcc ctg gcc gcc gcc gct gag gcc gat agt			864
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser			
	275	280	285
gag cac ccc gtg gcc cgc gcg atc gtg act gcc gcg gcc gca cac ccg			912
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala His Pro			
	290	295	300

gag gcc tcg cag cgt cag ctg cgc gca acc ggt ttc acc gcc gcc tcc Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser 305 310 315 320	960
ggc cgc ggg atc cgg gcc acc gtc gac ggt gcc gaa atc ctc gtg ggc Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly 325 330 335	1008
ggg ccg aac atg cta cgc gag ttc aat ctg acc acc ccg ggt gag ctc Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu 340 345 350	1056
gcc gac atc acc ggt tcc tgg gca cag cga ggt gcc gga gtg cta cat Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His 355 360 365	1104
gtc gtc cgc gac ggt gag atc atc ggt gcg gtg gca gtg gag gac aaa Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys 370 375 380	1152
atc cgc ccc gaa tcc cgc gcg gcg gta cgc gcc ctg cag gcc cgc ggg Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly 385 390 395 400	1200
gtg aag gtg gcg atg atc acc ggt gac gcc acc cag gtc gcc cag gca Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala 405 410 415	1248
gtg ggc aag gat ctg ggg atc gat gag gtc ttc gcc gag gtt ctg ccg Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro 420 425 430	1296
cag gac aag gac acc aag gtc acc cag ctg cag gag cgc ggt ctg agc Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser 435 440 445	1344
gtg gcc atg gtc ggc gac ggt gtc aat gac gcc ccg gcc ctg gcc ccg Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg 450 455 460	1392
gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg gag Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu 465 470 475 480	1440
tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc ccg gcc gtg ctg tcg Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser 485 490 495	1488
atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac ctg Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu 500 505 510	1536
gtc tgg gcg acc ggg tac aac atc gtg gcc gtt ccg ctg gcc gcc ggt Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly 515 520 525	1584
gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc atc Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile 530 535 540	1632

ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg cta 1680  
 Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu  
 545 550 555 560

cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg aag 1728  
 Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys  
 565 570 575

gag gag aag gct gct gtg agc tct gca gcc ccc gtc cgc tgactttcaa 1777  
 Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg  
 580 585

tgcttcattgg act 1790

<210> 22

<211> 589

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe  
 1 5 10 15

Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp  
 20 25 30

Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu  
 35 40 45

Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr  
 50 55 60

Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val  
 65 70 75 80

Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala  
 85 90 95

Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr  
 100 105 110

Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn  
 115 120 125

Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala  
 130 135 140

Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala  
 145 150 155 160

Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu  
 165 170 175

Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro  
 180 185 190

Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro  
 195 200 205

His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu

210	215	220
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu 225 230 235 240		
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu 245 250 255		
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile 260 265 270		
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Glu Ala Asp Ser 275 280 285		
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala His Pro 290 295 300		
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser 305 310 315 320		
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly 325 330 335		
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu 340 345 350		
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His 355 360 365		
Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys 370 375 380		
Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly 385 390 395 400		
Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala 405 410 415		
Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro 420 425 430		
Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser 435 440 445		
Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg 450 455 460		
Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu 465 470 475 480		
Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser 485 490 495		
Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu 500 505 510		
Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly 515 520 525		
Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile 530 535 540		

Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu  
545 550 555 560

Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys  
565 570 575

Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg  
580 585

<210> 23

<211> 807

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> RXA00002

<400> 23

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ggctgcagac aagctcgcgtg ctgaggattc tcacctgcac gtg ctg cac cgc gaa 115  
Val Leu His Arg Glu  
1 5  
ggc aag ggt ggc ctt ctt ggc gct tat atc gcc ggc ttc gag tgg ggc 163  
Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala Gly Phe Glu Trp Gly  
10 15 20  
cta gag aag gat tac cat gtt ctg tgc gaa atg gat gcc gac ggc tcc 211  
Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met Asp Ala Asp Gly Ser  
25 30 35  
cac gca cca gaa cag ctc cac ctc ttg ctt gag gaa att gaa aag ggc 259  
His Ala Pro Glu Gln Leu His Leu Leu Glu Glu Ile Glu Lys Gly  
40 45 50  
gca gat ctg gtc att ggc tcc cgc tac gta ccg ggt gga gag aca gtg 307  
Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Glu Thr Val  
55 60 65  
aac tgg cct gcc aac cgc gaa ctg ctg tcc cgc ttg ggc aac aag tac 355  
Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg Leu Gly Asn Lys Tyr  
70 75 80 85  
att tct gtt gcc ctg ggt gcc ggc atc aat gac atg act gcc ggc tac 403  
Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp Met Thr Ala Gly Tyr  
90 95 100  
cgt gct ttc cgg cgt gag ctg ctt gag cac ctc gac ttt gag gag ctt 451  
Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu Asp Phe Glu Glu Leu  
105 110 115  
tcc aac gcc gga tac atc ttc cag gtg gac gtt gcc ttc cgc gcc atc 499  
Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val Ala Phe Arg Ala Ile  
120 125 130  
aag gat ggc ttc gat gtc cgc gag gtt ccg atc acc ttc acc gag cgc 547

Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu Arg  
 135 140 145  
 gag ctt ggt gaa tcc aag ctg gac ggc tcc ttt gtc aag gat tcc ctg 595  
 Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser Leu  
 150 155 160 165  
 ctc gaa gta acc aag tgg gga gtg gct cac cgc tcc gag cag atc agc 643  
 Leu Glu Val Thr Lys Trp Gly Val Ala His Arg Ser Glu Gln Ile Ser  
 170 175 180  
 gat ttc aca tcg gaa gta tcc aag atc gcc tcc cgc acg gtc aag gac 691  
 Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser Arg Thr Val Lys Asp  
 185 190 195  
 atg gag ctt ggc cct aag gcc acc acg gcc aag aac gct gta ccg gac 739  
 Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys Asn Ala Val Pro Asp  
 200 205 210  
 ttc gtt tcc gaa gtc tct aac cta gct aaa ggc acc ttc aag aag 784  
 Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly Thr Phe Lys Lys  
 215 220 225  
 taactcgatg cccgcggcgt ctc 807

&lt;210&gt; 24

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 24

Val Leu His Arg Glu Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala  
 1 5 10 15  
 Gly Phe Glu Trp Gly Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met  
 20 25 30  
 Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Glu  
 35 40 45  
 Glu Ile Glu Lys Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro  
 50 55 60  
 Gly Gly Glu Thr Val Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg  
 65 70 75 80  
 Leu Gly Asn Lys Tyr Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp  
 85 90 95  
 Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu  
 100 105 110  
 Asp Phe Glu Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val  
 115 120 125  
 Ala Phe Arg Ala Ile Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile  
 130 135 140  
 Thr Phe Thr Glu Arg Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe  
 145 150 155 160

Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Val Ala His Arg  
 165 170 175

Ser Glu Gln Ile Ser Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser  
 180 185 190

Arg Thr Val Lys Asp Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys  
 195 200 205

Asn Ala Val Pro Asp Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly  
 210 215 220

Thr Phe Lys Lys  
 225

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 <211> 696  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(673)  
 <223> RXA00160

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ggccaatctg accatttttaa cctccataaa aaggattctc atg cta aac atc gca 115  
 Met Leu Asn Ile Ala  
 1 5

cgc aac cgc aac atg aag cgt cga cta gca att gct gct ttc gtc gcc 163  
 Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile Ala Ala Phe Val Ala  
 10 15 20

acc gca acc gct acc gcc acc atg gca cca gca tcc gcg caa acc gac 211  
 Thr Ala Thr Ala Thr Ala Thr Met Ala Pro Ala Ser Ala Gln Thr Asp  
 25 30 35

tac gca ggc ctt tcc tcc ggc gtt gcc gac acc gtc gca gaa gct gca 259  
 Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr Val Ala Glu Ala Ala  
 40 45 50

gga gtc gca acc acc gcc gtc gca cca gcc gcc acc gta gcg cgc cca 307  
 Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala Thr Val Ala Arg Pro  
 55 60 65

gca aac ggc acc ttc acc tca gga ttc gga cca cgt tgg gga acc ttc 355  
 Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro Arg Trp Gly Thr Phe  
 70 75 80 85

cac aac ggc atc gac atc gca aac tca atc ggc acc cca atc tac gcc 403  
 His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly Thr Pro Ile Tyr Ala  
 90 95 100

gtc atg gcc ggc act gtc atc agc tct ggc cca gca tcc ggc tat gga 451  
 Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro Ala Ser Gly Tyr Gly  
 105 110 115

cag tgg atc cgc atc cag cac gac gac gga tcc atc tcc atc tac gga 499  
Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser Ile Ser Ile Tyr Gly  
120 125 130

cac atg gaa tac ctc tac gtc tcc gtc ggc gaa cgc gtc gca gca ggc 547  
His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu Arg Val Ala Ala Gly  
135 140 145

cag gaa atc gca gga atg ggc agc caa gga ttc tcc acc ggc tcc cac 595  
Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe Ser Thr Gly Ser His  
150 155 160 165

ctc cac ttc gag atc cac cca gac ggc gtc acc cca gtc gac cca cag 643  
Leu His Phe Glu Ile His Pro Asp Gly Val Thr Pro Val Asp Pro Gln  
170 175 180

gca tgg ctc gca aac cac ggc atc tac gtt taagcgctag ccgttcgtgg gat 696  
Ala Trp Leu Ala Asn His Gly Ile Tyr Val  
185 190

<210> 26

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Met Leu Asn Ile Ala Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile  
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Ala Ala Phe Val Ala Thr Ala Thr Ala Thr Ala Thr Met Ala Pro Ala  
20 25 30

Ser Ala Gln Thr Asp Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr  
35 40 45

Val Ala Glu Ala Ala Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala  
50 55 60

Thr Val Ala Arg Pro Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro  
65 70 75 80

Arg Trp Gly Thr Phe His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly  
85 90 95

Thr Pro Ile Tyr Ala Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro  
100 105 110

Ala Ser Gly Tyr Gly Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser  
115 120 125

Ile Ser Ile Tyr Gly His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu  
130 135 140

Arg Val Ala Ala Gly Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe  
145 150 155 160

Ser Thr Gly Ser His Leu His Phe Glu Ile His Pro Asp Gly Val Thr  
165 170 175



Pro Val Asp Pro Gln Ala Trp Leu Ala Asn His Gly Ile Tyr Val  
 180 185 190

<210> 27  
 <211> 1063  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <221> CDS  
 <222> (90)..(1040)  
 <223> RXA00345

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 Met Ala Gly Met Lys Lys Leu Leu  
 1 5  
 tgg aca ctc ccc atc ctc cca ctg gta cta gct ggc tgc tca act gga 161  
 Trp Thr Leu Pro Ile Leu Pro Leu Val Leu Ala Gly Cys Ser Thr Gly  
 10 15 20  
 tca gca gat tcc gcg gat tcc acc aac gct gcc gga tcc aat tcc ctt 209  
 Ser Ala Asp Ser Ala Asp Ser Thr Asn Ala Ala Gly Ser Asn Ser Leu  
 25 30 35 40  
 aaa gtg gtc acc tcc acc cag gtg tgg gct gac gtc gcc gaa gct gtc 257  
 Lys Val Val Thr Ser Thr Gln Val Trp Ala Asp Val Ala Glu Ala Val  
 45 50 55  
 gcc cca gat gta gac att gaa gca att att acc ggt ggc gac atc gac 305  
 Ala Pro Asp Val Asp Ile Glu Ala Ile Ile Thr Gly Gly Asp Ile Asp  
 60 65 70  
 cct cat tcc ttc gag cct tcc gct acc gat atg gct aaa gtt tcc gaa 353  
 Pro His Ser Phe Glu Pro Ser Ala Thr Asp Met Ala Lys Val Ser Glu  
 75 80 85  
 gct gac atc att atc gtc ggt ggc ggc ggc tat gat tcc tgg ctc tac 401  
 Ala Asp Ile Ile Ile Val Gly Gly Gly Gly Tyr Asp Ser Trp Leu Tyr  
 90 95 100  
 ggc acc ttg gaa gac gat gat cgc atc atc cac gca ttg gat ctc tca 449  
 Gly Thr Leu Glu Asp Asp Asp Arg Ile Ile His Ala Leu Asp Leu Ser  
 105 110 115 120  
 gag cat gac cac agc gag cat gat gat cac gag cac gaa gcc gaa gaa 497  
 Glu His Asp His Ser Glu His Asp Asp His Glu His Glu Ala Glu Glu  
 125 130 135  
 gcc cac gaa cac gac cac gat gaa gag ggc cac gat cat gac gtc gac 545  
 Ala His Glu His Asp His Asp Glu Glu Gly His Asp His Asp Val Asp  
 140 145 150  
 aac gag cac gtc tgg tac tcc act gaa tac gtc tct gag gta gct gaa 593  
 Asn Glu His Val Trp Tyr Ser Thr Glu Tyr Val Ser Glu Val Ala Glu  
 155 160 165

gag ttc gca gaa aaa gtc acc gag ctt gat ccc gag gca cag gcc gat 641  
 Glu Phe Ala Glu Lys Val Thr Glu Leu Asp Pro Glu Ala Gln Ala Asp  
 170 175 180

gca acg gct gtg acc acc aag atg gac gag ctg cac aat cag att cac 689  
 Ala Thr Ala Val Thr Thr Lys Met Asp Glu Leu His Asn Gln Ile His  
 185 190 195 200

gat ctt cca gca gtt cgc att gct cag acc gag ccg atc gcc gat cac 737  
 Asp Leu Pro Ala Val Arg Ile Ala Gln Thr Glu Pro Ile Ala Asp His  
 205 210 215

att ttg tcc cac tcc gac atg gtg gaa tcc acc cct gag ggt tac cgc 785  
 Ile Leu Ser His Ser Asp Met Val Glu Ser Thr Pro Glu Gly Tyr Arg  
 220 225 230

gca acc acg ttg agc gag agc gag cca acc gca gca gat gtt gcg tcg 833  
 Ala Thr Thr Leu Ser Glu Ser Glu Pro Thr Ala Ala Asp Val Ala Ser  
 235 240 245

ttc cag gat gca att aac aac ggt gac ctc gat gtt ttg atc tac aac 881  
 Phe Gln Asp Ala Ile Asn Asn Gly Asp Leu Asp Val Leu Ile Tyr Asn  
 250 255 260

cca cag tcc gcg tcg act gtc gcg acc agc ttg aag gat ttg gca gaa 929  
 Pro Gln Ser Ala Ser Thr Val Ala Thr Ser Leu Lys Asp Leu Ala Glu  
 265 270 275 280

gaa aaa ggc atc cca gtt gtt gag atc tat gag acc cct caa aac acc 977  
 Glu Lys Gly Ile Pro Val Val Glu Ile Tyr Glu Thr Pro Gln Asn Thr  
 285 290 295

gag aat ttc ctc gat gca ttc acc aag gca gtt gat gat ctc acc gct 1025  
 Glu Asn Phe Leu Asp Ala Phe Thr Lys Ala Val Asp Asp Leu Thr Ala  
 300 305 310

gcc act aac cag gtt tagaattatt taaatgctgt tga 1063  
 Ala Thr Asn Gln Val  
 315

&lt;210&gt; 28

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 28

Met Ala Gly Met Lys Lys Leu Leu Trp Thr Leu Pro Ile Leu Pro Leu  
 1 5 10 15

Val Leu Ala Gly Cys Ser Thr Gly Ser Ala Asp Ser Ala Asp Ser Thr  
 20 25 30

Asn Ala Ala Gly Ser Asn Ser Leu Lys Val Val Thr Ser Thr Gln Val  
 35 40 45

Trp Ala Asp Val Ala Glu Ala Val Ala Pro Asp Val Asp Ile Glu Ala  
 50 55 60

Ile Ile Thr Gly Gly Asp Ile Asp Pro His Ser Phe Glu Pro Ser Ala  
 65 70 75 80

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<400> 29
ctgtacagat cgcggtctat ggtgctaata tcctaaatac ttgaatgacc atttcatgat 60
ccattcacaa aaactttccc aaacaaggac gtatttgaaa atg aaa ctt cgt cgc 115
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	Met	Lys	Leu	Arg	Arg	
	1				5	
atc aca acc acc gcc atc gct ggc ctc ttc gcc gca acc gca ctt gtt						163
Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala Ala Thr Ala Leu Val						
	10			15	20	
gcc tgt ggc tcc gat tcc gat gga agc agc acc act gtt gct gaa ggc						211
Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr Thr Val Ala Glu Gly						
	25			30	35	
acc gaa ggc gtg acc atc cgc atc ggc acc acc gac gct gcg aag gaa						259
Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr Asp Ala Ala Lys Glu						
	40			45	50	
gca tgg acc gta ttc gaa gac aag gca gct gaa gag ggc atc acc ctc						307
Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu Glu Gly Ile Thr Leu						
	55			60	65	
gac atc gtt cct ttc tct gac tac tcc acc cca aat gag gct ctt gcc						355
Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro Asn Glu Ala Leu Ala						
	70			75	80	85
cag gat cag ctg gac gtt aac ctc ttc cag cac ctg aag ttc ctg gct						403
Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His Leu Lys Phe Leu Ala						
	90			95	100	
gag tac aac gtc ggc tcc ggc gca gac ctc acc cca gtt ggc tcc agc						451
Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr Pro Val Gly Ser Ser						
	105			110	115	
gaa atc gtg cca ctg gca cta ttc tgg aag gac cac gac tcc atc gac						499
Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp His Asp Ser Ile Asp						
	120			125	130	
ggc att gac ggc gag tcc gtt gcc atc cct aac gat cct tcc aac cag						547
Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn Asp Pro Ser Asn Gln						
	135			140	145	
ggc cgc gcc atc aac gtt ctc gtt cag gca ggt ctg gtc acc ctg aag						595
Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly Leu Val Thr Leu Lys						
	150			155	160	165
acc cca ggt ctg gtc acc cca gct cca gtc gat atc gac gag gca gct						643
Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp Ile Asp Glu Ala Ala						
	170			175	180	
tcc aag gtt tcc gtc atc cca gtc gac gca gct cag gca cca acc gct						691
Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala Gln Ala Pro Thr Ala						
	185			190	195	
tac cag gag ggt cgc cca gcg atc atc aac aac tcc ttc ctt gac cgc						739
Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn Ser Phe Leu Asp Arg						
	200			205	210	
gca ggc atc gat cca aac ctc gcg gtc ttc gaa gat gat cct gag tct						787
Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu Asp Asp Pro Glu Ser						
	215			220	225	
gaa gaa gca gag cca tac atc aac gtc ttc gtc acc aag gct gag gac						835
Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val Thr Lys Ala Glu Asp						

230                                      235                                      240                                      245

aag gac gat gcc aac atc gcc cgc ctc gtt gag ctg tgg cac gac cca      883  
 Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu Leu Trp His Asp Pro  
    250                                      255                                      260

gag gtt ctg gct gca gta gac cgc gac tct gag ggc acc tcc gtc cca      931  
 Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu Gly Thr Ser Val Pro  
    265                                      270                                      275

gtt gat cgt cca gga gct gac ctt cag gaa atc ctt gat cgc ctt gag      979  
 Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile Leu Asp Arg Leu Glu  
    280                                      285                                      290

gct gat cag gaa aac gca taatctcttt tgagttcttt gca                      1020  
 Ala Asp Gln Glu Asn Ala  
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<210> 30  
 <211> 299  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 30  
 Met Lys Leu Arg Arg Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala  
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Ala Thr Ala Leu Val Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr  
    20                                      25                                      30

Thr Val Ala Glu Gly Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr  
    35                                      40                                      45

Asp Ala Ala Lys Glu Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu  
    50                                      55                                      60

Glu Gly Ile Thr Leu Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro  
     65                                      70                                      75                                      80

Asn Glu Ala Leu Ala Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His  
    85                                      90                                      95

Leu Lys Phe Leu Ala Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr  
    100                                      105                                      110

Pro Val Gly Ser Ser Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp  
    115                                      120                                      125

His Asp Ser Ile Asp Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn  
    130                                      135                                      140

Asp Pro Ser Asn Gln Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly  
     145                                      150                                      155                                      160

Leu Val Thr Leu Lys Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp  
    165                                      170                                      175

Ile Asp Glu Ala Ala Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala  
    180                                      185                                      190

Gln Ala Pro Thr Ala Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn  
 195 200 205

Ser Phe Leu Asp Arg Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu  
 210 215 220

Asp Asp Pro Glu Ser Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val  
 225 230 235 240

Thr Lys Ala Glu Asp Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu  
 245 250 255

Leu Trp His Asp Pro Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu  
 260 265 270

Gly Thr Ser Val Pro Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile  
 275 280 285

Leu Asp Arg Leu Glu Ala Asp Gln Glu Asn Ala  
 290 295

<210> 31  
 <211> 771  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(748)  
 <223> RXA00482

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actattgagt taatataaac atgaagaaag gatttgcttt atg cgc att tca agc 115  
 Met Arg Ile Ser Ser  
 1 5

aaa ctt gtc acc aca gca cta ctc gca gcc att tca ctt ttc ggg ata 163  
 Lys Leu Val Thr Thr Ala Leu Leu Ala Ala Ile Ser Leu Phe Gly Ile  
 10 15 20

tcc acg gca caa gcc caa gac att ttt gac ggc gga cga ctt gca ggt 211  
 Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly Gly Arg Leu Ala Gly  
 25 30 35

ggc tcc tcg cag gta tct aac cta agt tcg gtt cct gaa aac cta gcg 259  
 Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val Pro Glu Asn Leu Ala  
 40 45 50

ctg ccc gaa att gaa aat agc att gac cta gaa cgc tac aaa ggc aag 307  
 Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu Arg Tyr Lys Gly Lys  
 55 60 65

tgg tat caa gtc gca gca att ccc caa cca ttc tct tta cag tgc tca 355  
 Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe Ser Leu Gln Cys Ser  
 70 75 80 85

cat gac gtt acc gct gat tac ggc gtg atc gac tcg gac aca atc tct 403  
 His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp Ser Asp Thr Ile Ser

90										95					100					
gta	aca	aat	aag	tgt	ggc	act	ttc	ttt	ggg	cct	tca	gtt	att	gaa	ggc	451				
Val	Thr	Asn	Lys	Cys	Gly	Thr	Phe	Phe	Gly	Pro	Ser	Val	Ile	Glu	Gly					
			105							110				115						
agc	gct	aaa	gta	gtt	tcc	aat	gct	tca	tta	aag	gtt	agc	ttc	cca	ggc	499				
Ser	Ala	Lys	Val	Val	Ser	Asn	Ala	Ser	Leu	Lys	Val	Ser	Phe	Pro	Gly					
			120							125				130						
att	cca	ttt	cag	agt	gaa	gac	aat	caa	gca	aac	tac	cgc	gtg	acc	tat	547				
Ile	Pro	Phe	Gln	Ser	Glu	Asp	Asn	Gln	Ala	Asn	Tyr	Arg	Val	Thr	Tyr					
			135							140				145						
atc	gaa	gat	gat	tat	tca	cta	gca	atc	gtc	ggc	agc	cca	agc	cgg	tcc	595				
Ile	Glu	Asp	Asp	Tyr	Ser	Leu	Ala	Ile	Val	Gly	Ser	Pro	Ser	Arg	Ser					
			150							155				160						
tca	gga	ttt	ata	cta	tcc	cgc	acg	cca	cag	ctc	agt	agt	gac	caa	tgg	643				
Ser	Gly	Phe	Ile	Leu	Ser	Arg	Thr	Pro	Gln	Leu	Ser	Ser	Asp	Gln	Trp					
			170							175				180						
tct	cac	gtt	cgg	aac	att	aca	gag	gac	agt	ggg	tgg	tgg	cca	tgc	gca	691				
Ser	His	Val	Arg	Asn	Ile	Thr	Glu	Asp	Ser	Gly	Trp	Trp	Pro	Cys	Ala					
			185							190				195						
ttc	att	aca	gtc	cca	gcg	aca	ggc	ggc	tta	aac	acc	gcc	act	ccg	ctc	739				
Phe	Ile	Thr	Val	Pro	Ala	Thr	Gly	Gly	Leu	Asn	Thr	Ala	Thr	Pro	Leu					
			200							205				210						
tgc	aca	ctt	taattaacgt	agatggcat	cta											771				
Cys	Thr	Leu																		
			215																	

&lt;210&gt; 32

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 32

Met	Arg	Ile	Ser	Ser	Lys	Leu	Val	Thr	Thr	Ala	Leu	Leu	Ala	Ala	Ile
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Ser	Leu	Phe	Gly	Ile	Ser	Thr	Ala	Gln	Ala	Gln	Asp	Ile	Phe	Asp	Gly
		20						25					30		
Gly	Arg	Leu	Ala	Gly	Gly	Ser	Ser	Gln	Val	Ser	Asn	Leu	Ser	Ser	Val
		35					40					45			
Pro	Glu	Asn	Leu	Ala	Leu	Pro	Glu	Ile	Glu	Asn	Ser	Ile	Asp	Leu	Glu
	50					55					60				
Arg	Tyr	Lys	Gly	Lys	Trp	Tyr	Gln	Val	Ala	Ala	Ile	Pro	Gln	Pro	Phe
65					70					75					80
Ser	Leu	Gln	Cys	Ser	His	Asp	Val	Thr	Ala	Asp	Tyr	Gly	Val	Ile	Asp
				85					90					95	
Ser	Asp	Thr	Ile	Ser	Val	Thr	Asn	Lys	Cys	Gly	Thr	Phe	Phe	Gly	Pro
			100					105						110	

Ser Val Ile Glu Gly Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys  
 115 120 125

Val Ser Phe Pro Gly Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn  
 130 135 140

Tyr Arg Val Thr Tyr Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly  
 145 150 155 160

Ser Pro Ser Arg Ser Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu  
 165 170 175

Ser Ser Asp Gln Trp Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly  
 180 185 190

Trp Trp Pro Cys Ala Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn  
 195 200 205

Thr Ala Thr Pro Leu Cys Thr Leu  
 210 215

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1735)  
 <223> RXN01164

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 Val Thr Leu Phe Val  
 1 5

cgg ctg gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat 163  
 Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn  
 10 15 20

gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211  
 Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe  
 25 30 35

ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg 259  
 Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg  
 40 45 50

aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca 307  
 Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro  
 55 60 65

act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca 355  
 Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr  
 70 75 80 85

tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct 403



Tyr	Leu	Gln	Leu	Leu	Pro	Trp	Ile	Gly	Glu	Phe	Val	Gly	Ser	Leu	Pro		
				90					95					100			
tat	gtc	gcg	ttg	tca	gtt	gtc	gag	gcg	ctt	tat	tcc	att	gct	ctt	ggt	451	
Tyr	Val	Ala	Leu	Ser	Val	Val	Glu	Ala	Leu	Tyr	Ser	Ile	Ala	Leu	Gly		
			105					110					115				
gct	ttc	ggc	gtg	ctc	att	gcg	cgt	tgg	agg	gac	tgg	aag	gtt	ctc	ctg	499	
Ala	Phe	Gly	Val	Leu	Ile	Ala	Arg	Trp	Arg	Asp	Trp	Lys	Val	Leu	Leu		
		120					125					130					
ttt	ccg	gcg	atg	tat	gtg	gct	gtg	gag	tat	cta	aga	agc	tcg	tgg	cca	547	
Phe	Pro	Ala	Met	Tyr	Val	Ala	Val	Glu	Tyr	Leu	Arg	Ser	Ser	Trp	Pro		
	135					140					145						
ttt	gat	gga	ttc	gcg	tgg	gtt	cgc	ctg	gca	tgg	ggt	caa	att	aac	ggt	595	
Phe	Asp	Gly	Phe	Ala	Trp	Val	Arg	Leu	Ala	Trp	Gly	Gln	Ile	Asn	Gly		
150					155				160					165			
ccg	ttg	gct	aat	ctc	gca	gcg	ctt	ggt	ggg	gta	gcg	ttt	gtc	act	ttt	643	
Pro	Leu	Ala	Asn	Leu	Ala	Ala	Leu	Gly	Gly	Val	Ala	Phe	Val	Thr	Phe		
				170					175					180			
tcc	acg	gtg	ctg	gct	gcc	gtg	ggt	gtg	gcc	atg	gtg	att	att	tcc	aag	691	
Ser	Thr	Val	Leu	Ala	Ala	Val	Gly	Val	Ala	Met	Val	Ile	Ile	Ser	Lys		
			185					190					195				
aag	cga	ctg	gcc	ggc	gca	atc	atc	acc	gcg	agt	gtg	att	gct	atc	ggc	739	
Lys	Arg	Leu	Ala	Gly	Ala	Ile	Ile	Thr	Ala	Ser	Val	Ile	Ala	Ile	Gly		
		200					205					210					
gcg	gtg	tca	tcc	ctg	tac	gtt	gac	cgc	aat	ggc	acg	agc	gat	gaa	agc	787	
Ala	Val	Ser	Ser	Leu	Tyr	Val	Asp	Arg	Asn	Gly	Thr	Ser	Asp	Glu	Ser		
	215					220					225						
atc	gaa	gta	gcc	gca	att	cag	ggc	aat	gtg	cct	cgg	atg	gga	ttg	gac	835	
Ile	Glu	Val	Ala	Ala	Ile	Gln	Gly	Asn	Val	Pro	Arg	Met	Gly	Leu	Asp		
230					235					240				245			
ttc	aat	gca	cag	cgc	cgc	gcg	gtg	ctg	gcg	aat	cac	gca	cgg	gaa	acc	883	
Phe	Asn	Ala	Gln	Arg	Arg	Ala	Val	Leu	Ala	Asn	His	Ala	Arg	Glu	Thr		
			250						255					260			
ctc	aag	ctg	gat	gaa	caa	gtg	gat	ttg	gtg	atc	tgg	ccg	gag	aat	tcc	931	
Leu	Lys	Leu	Asp	Glu	Gln	Val	Asp	Leu	Val	Ile	Trp	Pro	Glu	Asn	Ser		
			265					270					275				
tca	gac	gtc	aac	cca	ttt	tcc	gat	gca	caa	gca	aga	gcc	att	atc	gat	979	
Ser	Asp	Val	Asn	Pro	Phe	Ser	Asp	Ala	Gln	Ala	Arg	Ala	Ile	Ile	Asp		
		280					285					290					
gga	gca	gtg	gaa	cat	gtt	cag	gca	cct	att	ttg	gtg	ggc	acg	atc	acc	1027	
Gly	Ala	Val	Glu	His	Val	Gln	Ala	Pro	Ile	Leu	Val	Gly	Thr	Ile	Thr		
	295					300					305						
gtc	gat	gag	gtt	ggt	cca	cgc	aac	acc	atg	cag	gta	ttt	gat	cct	gtt	1075	
Val	Asp	Glu	Val	Gly	Pro	Arg	Asn	Thr	Met	Gln	Val	Phe	Asp	Pro	Val		
310					315					320				325			
gaa	ggt	gcc	gcg	gag	tac	cac	aat	aag	aag	ttc	ttg	cag	ccg	ttt	ggt	1123	
Glu	Gly	Ala	Ala	Glu	Tyr	His	Asn	Lys	Lys	Phe	Leu	Gln	Pro	Phe	Gly		

330	335	340	
gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt			1171
Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val			
345	350	355	
gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag			1219
Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu			
360	365	370	
atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg			1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr			
375	380	385	
tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat			1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn			
390	395	400	405
ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc			1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe			
410	415	420	
acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc			1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile			
425	430	435	
gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct			1459
Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala			
440	445	450	
atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag			1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu			
455	460	465	
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc			1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile			
470	475	480	485
gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt			1603
Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Val Ile Ile Gly			
490	495	500	
gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct			1651
Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser			
505	510	515	
gcg aaa ggt tcc gct cgg ccc gca caa gtt cgg gtt aag aag gtg cct			1699
Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg Val Lys Lys Val Pro			
520	525	530	
gcg aaa aag gca gca act aat cgt cga aaa gta aaa taacgctc			1745
Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val Lys			
535	540	545	
ccgaaggac gag			1758

&lt;210&gt; 34

&lt;211&gt; 545

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 34

Val Thr Leu Phe Val Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe  
 1 5 10 15  
 Val Phe Ala Ser Asn Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val  
 20 25 30  
 Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val  
 35 40 45  
 Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln  
 50 55 60  
 Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val  
 65 70 75 80  
 His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe  
 85 90 95  
 Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr  
 100 105 110  
 Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp  
 115 120 125  
 Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu  
 130 135 140  
 Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp  
 145 150 155 160  
 Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val  
 165 170 175  
 Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met  
 180 185 190  
 Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser  
 195 200 205  
 Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly  
 210 215 220  
 Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro  
 225 230 235 240  
 Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn  
 245 250 255  
 His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile  
 260 265 270  
 Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala  
 275 280 285  
 Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu  
 290 295 300  
 Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln  
 305 310 315 320

Lys  
545

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<222> (101)..(1675)
<223> FRXA01164
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tttcaacaaa ggtaaagatg aatccgacgg tgagaaataa gtg aca ctg ttt gtt 115
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	Val	Thr	Leu	Phe	Val	
	1				5	
cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat						163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn						
	10				20	
gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt						211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe						
	25				35	
ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg						259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg						
	40				50	
aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca						307
Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro						
	55				65	
act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca						355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr						
	70				80	85
tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct						403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro						
	90				95	100
tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt						451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly						
	105				110	115
gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg						499
Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp Trp Lys Val Leu Leu						
	120				125	130
ttt ccg gcg atg tat gtg gct gtg gag tat cta aga agc tcg tgg cca						547
Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro						
	135				140	145
ttt gat gga ttc gcg tgg gtt cgc ctg gca tgg ggt caa att aac ggt						595
Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp Gly Gln Ile Asn Gly						
	150				155	160
ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt						643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe						
	170				175	180
tcc acg gtg ctg gct gcc gtg ggt gtg gcc atg gtg att att tcc aag						691
Ser Thr Val Leu Ala Ala Val Gly Val Ala Met Val Ile Ile Ser Lys						
	185				190	195
aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc						739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly						
	200				205	210
gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc						787
Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly Thr Ser Asp Glu Ser						
	215				220	225
atc gaa gta gcc gca att cag ggc aat gtg cct cgg atg gga ttg gac						835
Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro Arg Met Gly Leu Asp						

230	235	240	245	
ttc aat gca cag cgc cgc gcg gtg ctg gcg aat cac gca cgg gaa acc Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn His Ala Arg Glu Thr	250	255	260	883
ctc aag ctg gat gaa caa gtg gat ttg gtg atc tgg ccg gag aat tcc Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile Trp Pro Glu Asn Ser	265	270	275	931
tca gac gtc aac cca ttt tcc gat gca caa gca aga gcc att atc gat Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala Arg Ala Ile Ile Asp	280	285	290	979
gga gca gtg gaa cat gtt cag gca cct att ttg gtg ggc acg atc acc Gly Ala Val Glu His Val Gln Ala Pro Ile Leu Val Gly Thr Ile Thr	295	300	305	1027
gtc gat gag gtt ggt cca cgc aac acc atg cag gta ttt gat cct gtt Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln Val Phe Asp Pro Val	310	315	320	1075
gaa ggt gcc gcg gag tac cac aat aag aag ttc ttg cag ccg ttt ggt Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe Leu Gln Pro Phe Gly	330	335	340	1123
gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val	345	350	355	1171
gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu	360	365	370	1219
atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acc Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr	375	380	385	1267
tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn	390	395	400	1315
ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe	410	415	420	1363
acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile	425	430	435	1411
gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala	440	445	450	1459
atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu	455	460	465	1507
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile	470	475	480	1555

gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt 1603  
 Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly  
 490 495 500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct 1651  
 Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser  
 505 510 515

gcg aaa ggt tcc gct cgg ccc gca 1675  
 Ala Lys Gly Ser Ala Arg Pro Ala  
 520 525

<210> 36

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Val Thr Leu Phe Val Arg Leu Ala Leu Ala Val Gly Gly Leu Phe  
 1 5 10 15

Val Phe Ala Ser Asn Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val  
 20 25 30

Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val  
 35 40 45

Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln  
 50 55 60

Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val  
 65 70 75 80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe  
 85 90 95

Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr  
 100 105 110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp  
 115 120 125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu  
 130 135 140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp  
 145 150 155 160

Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val  
 165 170 175

Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met  
 180 185 190

Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser  
 195 200 205

Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly  
 210 215 220

Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro  
 225 230 235 240  
 Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn  
 245 250 255  
 His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile  
 260 265 270  
 Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala  
 275 280 285  
 Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu  
 290 295 300  
 Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln  
 305 310 315 320  
 Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe  
 325 330 335  
 Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile  
 340 345 350  
 Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly  
 355 360 365  
 Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr  
 370 375 380  
 Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg  
 385 390 395 400  
 Asp Ala Ile Ala Asn Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn  
 405 410 415  
 Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser  
 420 425 430  
 Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr  
 435 440 445  
 Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn  
 450 455 460  
 Thr Arg Ile Phe Glu Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys  
 465 470 475 480  
 Asp Thr Val Thr Ile Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu  
 485 490 495  
 Leu Val Ile Ile Gly Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn  
 500 505 510  
 Ser Arg Ser Lys Ser Ala Lys Gly Ser Ala Arg Pro Ala  
 515 520 525

&lt;210&gt; 37

&lt;211&gt; 933



ctc tcc aac gct ggg tac att ttc caa gtt gag att gcc tac cgt gca 691  
Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu Ile Ala Tyr Arg Ala

185	190	195	
gtt gaa gcc gga ttc gat gtt cgt gaa gtt ccc atc act ttc acc gag			739
Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu			
200	205	210	
cgt gag atc ggc gaa tcc aag ctg gac ggc agc ttt gtc aag gat tcc			787
Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser			
215	220	225	
ctg ctc gag gta acc aag tgg ggc ctc aag cac cgc ggt ggc cag gcc			835
Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His Arg Gly Gly Gln Ala			
230	235	240	245
aag gaa ctg tcc aag gaa atg gtc ggc ctg ctg aac tat gag tgg aag			883
Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu Asn Tyr Glu Trp Lys			
250	255	260	
cac ttc aaa aag cgc aac acc tgg ctc taaactgctt gccggtagt gaa			933
His Phe Lys Lys Arg Asn Thr Trp Leu			
265	270		

&lt;210&gt; 38

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

Met Ser Ser Glu Ala Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr	
1 5 10 15	
Tyr Asn Glu Leu Glu Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr	
20 25 30	
Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser Pro Asp	
35 40 45	
Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile	
50 55 60	
Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met	
65 70 75 80	
Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu	
85 90 95	
Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu	
100 105 110	
Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val	
115 120 125	
Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser	
130 135 140	
Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr	
145 150 155 160	
Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala	
165 170 175	

Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu  
 180 185 190  
 Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro  
 195 200 205  
 Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser  
 210 215 220  
 Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His  
 225 230 235 240  
 Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu  
 245 250 255  
 Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu  
 260 265 270

<210> 39  
 <211> 743  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(720)  
 <223> FRXA01168

<400> 39  
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 Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser  
 1 5 10 15  
 cca gac ggc acc ggc gag cgc gca gac aag ctt gct gct gac gac gac 96  
 Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp  
 20 25 30  
 cac att ttt gtc ctc cac cgc gaa ggc aaa ggc ggc ctg tgc gca gag 144  
 His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu  
 35 40 45  
 tac atg gct ggc ttc cag tgg ggc ctg gag cgc gac tac cag gtc ctg 192  
 Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu  
 50 55 60  
 tgc gaa atg gac gcc gac ggc tcc cac gca cca gaa cag ctg cac ctg 240  
 Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu  
 65 70 75 80  
 ctg ctc gct gag atc acc aat ggc gct gac ctg gtc atc ggc tcg cgc 288  
 Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg  
 85 90 95  
 tac gtg cca ggc ggc cgc gta gtc aac tgg ccc aag aac cgt tgg ctc 336  
 Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu  
 100 105 110  
 ttg tcc aag ggc ggc aac gtc tac atc agc gtc gcg ctc ggc gcc ggc 384  
 Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly

115	120	125	
ttg acc gat atg acc gca ggg tac cgc gct ttt cga cgt gaa gtg cta			432
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu			
130	135	140	
gaa gca ctg ccg ctt gat gag ctc tcc aac gct ggg tac att ttc caa			480
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln			
145	150	155	160
gtt gag att gcc tac cgt gca gtt gaa gcc gga ttc gat gtt cgt gaa			528
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu			
	165	170	175
gtt ccc atc act ttc acc gag cgt gag atc ggc gaa tcc aag ctg gac			576
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp			
	180	185	190
ggc agc ttt gtc aag gat tcc ctg ctc gag gta acc aag tgg ggc ctc			624
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu			
	195	200	205
aag cac cgc ggt ggc cag gcc aag gaa ctg tcc aag gaa atg gtc ggc			672
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly			
	210	215	220
ctg ctg aac tat gag tgg aag cac ttc aaa aag cgc aac acc tgg ctc			720
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu			
225	230	235	240
taaactgctt gccggtagt gaa			743

&lt;210&gt; 40

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser
1 5 10 15

Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
20 25 30

His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
35 40 45

Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
50 55 60

Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
65 70 75 80

Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
85 90 95

Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
100 105 110

Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly
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115	120	125
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu		
130	135	140
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln		
145	150	155
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu		
	165	170
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp		
	180	185
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu		
	195	200
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly		
	210	215
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu		
	225	230
		235
		240

<210> 41  
 <211> 1293  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1270)  
 <223> RXN02062

<400> 41  
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 Met Arg Val Gly Met  
 1 5  
 atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163  
 Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His  
 10 15 20  
 gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt 211  
 Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val  
 25 30 35  
 cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc 259  
 His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly  
 40 45 50  
 gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc 307  
 Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser  
 55 60 65  
 acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac 355  
 Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His  
 70 75 80 85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc	403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu	
90 95 100	
cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc	451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg	
105 110 115	
cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg	499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp	
120 125 130	
tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg	547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser	
135 140 145	
gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg	595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro	
150 155 160 165	
gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag	643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln	
170 175 180	
cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta	691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu	
185 190 195	
ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc	739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr	
200 205 210	
cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac	787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp	
215 220 225	
gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa	835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu	
230 235 240 245	
atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc	883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg	
250 255 260	
gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa	931
Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln	
265 270 275	
gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag	979
Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu	
280 285 290	
cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt	1027
Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val	
295 300 305	
gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc	1075
Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr	
310 315 320 325	
acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag	1123

Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu  
 330 335 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171  
 Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr  
 345 350 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219  
 Ala Ala Lys Phe Gly Leu Ala Glu Arg Glu Arg Ala Ile Asn Asp Phe  
 360 365 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267  
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu  
 375 380 385

atg taaaaccgaa agccggggaa cct 1293  
 Met  
 390

&lt;210&gt; 42

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly  
 1 5 10 15

Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile  
 20 25 30

Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly  
 35 40 45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala  
 50 55 60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn  
 65 70 75 80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His  
 85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser  
 100 105 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr  
 115 120 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala  
 130 135 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr  
 145 150 155 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp  
 165 170 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser  
 180 185 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe  
195 200 205

Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala  
210 215 220

Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala  
225 230 235 240

Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu  
245 250 255

Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly  
260 265 270

Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys  
275 280 285

Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala  
290 295 300

Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val  
305 310 315 320

Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp  
325 330 335

Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val  
340 345 350

Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg  
355 360 365

Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp  
370 375 380

Val Tyr Lys Ser Leu Met  
385 390

<210> 43

<211> 1293

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1270)

<223> FRXA02062

<400> 43

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tcgctgcgca actgttttta gatggctaatt ctttgaaatt atg aga gtc gga atg 115  
Met Arg Val Gly Met  
1 5

atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163  
Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His  
10 15 20



gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt	211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val	
25 30 35	
cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc	259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly	
40 45 50	
gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc	307
Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser	
55 60 65	
acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac	355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His	
70 75 80 85	
tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc	403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu	
90 95 100	
cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc	451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg	
105 110 115	
cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg	499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp	
120 125 130	
tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tgc	547
Ser Glu Lys Asn Ala Met Tyr Ala Asp Ala Val Ile Ala Val Ser	
135 140 145	
gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg	595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro	
150 155 160 165	
gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag	643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln	
170 175 180	
cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta	691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu	
185 190 195	
ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc	739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr	
200 205 210	
cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac	787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp	
215 220 225	
gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa	835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu	
230 235 240 245	
atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc	883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg	
250 255 260	

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His  
85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser  
 100 105 110  
 Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr  
 115 120 125  
 Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala  
 130 135 140  
 Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr  
 145 150 155 160  
 Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp  
 165 170 175  
 Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser  
 180 185 190  
 Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe  
 195 200 205  
 Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala  
 210 215 220  
 Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala  
 225 230 235 240  
 Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu  
 245 250 255  
 Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly  
 260 265 270  
 Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys  
 275 280 285  
 Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala  
 290 295 300  
 Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val  
 305 310 315 320  
 Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp  
 325 330 335  
 Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val  
 340 345 350  
 Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg  
 355 360 365  
 Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp  
 370 375 380  
 Val Tyr Lys Ser Leu Met  
 385 390

<210> 45  
 <211> 498  
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RXA02222

<400> 45

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aagattgcaa aaaccttgaa aaagtgtatg gcagcgaatg ttg ggt cga cct ccc 115
                                   Leu Gly Arg Pro Pro
                                   1 5
cca gga gac gtt cat act ctc cta gac gat atc gga gca gag gaa tct 163
Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile Gly Ala Glu Glu Ser
                                   10 15 20
gaa gca gat aaa gtt cca att gaa tgg caa aac gcc ctg act aag gca 211
Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn Ala Leu Thr Lys Ala
                                   25 30 35
gac agg tat gca aac cgg caa cac atg tct cag gca cga ctc tat cgc 259
Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln Ala Arg Leu Tyr Arg
                                   40 45 50
caa tta acc agt gat gtt gga gag ggc ttc act gaa gaa gct gcc caa 307
Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr Glu Glu Ala Ala Gln
                                   55 60 65
tac gca atc gaa aat gtg aac gca gac tgg aac gct aac gcc cta gta 355
Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn Ala Asn Ala Leu Val
                                   70 75 80 85
aaa gca aga aat tac cag gag cgc caa gca atg tca gta gac cgc att 403
Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met Ser Val Asp Arg Ile
                                   90 95 100
tac agg caa ctt act agt gaa cac ggt gaa ggg ttt acc cca gag cag 451
Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly Phe Thr Pro Glu Gln
                                   105 110 115
gca caa tac gcg atc gac aac cta taaggcataa agatcctagt att 498
Ala Gln Tyr Ala Ile Asp Asn Leu
                                   120 125
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<210> 46

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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Leu Gly Arg Pro Pro Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile
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Gly Ala Glu Glu Ser Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn
 20 25 30
Ala Leu Thr Lys Ala Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln
 35 40 45
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Ala Arg Leu Tyr Arg Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr  
 50 55 60

Glu Glu Ala Ala Gln Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn  
 65 70 75 80

Ala Asn Ala Leu Val Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met  
 85 90 95

Ser Val Asp Arg Ile Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly  
 100 105 110

Phe Thr Pro Glu Gln Ala Gln Tyr Ala Ile Asp Asn Leu  
 115 120 125

<210> 47

<211> 1344

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1321)

<223> RXA02313

<400> 47

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ttaactgcga tgtaggcatg atgtggagat aataaggccc atg cgg gta gca att 115  
 Met Arg Val Ala Ile  
 1 5

gtt gca gag tcg ttc ctt cca aat gtc aac gga gtc acc aac tcg gtg 163  
 Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly Val Thr Asn Ser Val  
 10 15 20

ctc cgg gtg ttg gag cat ttg aaa gcc aac gga cac gac gcg ctc gtc 211  
 Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly His Asp Ala Leu Val  
 25 30 35

atc gcg ccg ggt gcc cgg gat ttt gaa gaa gaa atc ggc cac tac ctg 259  
 Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu Ile Gly His Tyr Leu  
 40 45 50

ggc ttt gaa att gtg cgc gtc ccc acc gtt cgg gtc cca ctg att gat 307  
 Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg Val Pro Leu Ile Asp  
 55 60 65

tca ctg ccc atc ggt gtt cct ctg ccc tca gtt acc tct gtg ctg cgc 355  
 Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val Thr Ser Val Leu Arg  
 70 75 80 85

gag tac aac cca gac atc att cac ctg gca tcc cca ttt gtg ctc ggt 403  
 Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser Pro Phe Val Leu Gly  
 90 95 100

gga gcg gca gca ttc gca gca agg cag ctg cgc atc cca gca att gct 451  
 Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg Ile Pro Ala Ile Ala  
 105 110 115

atc tat caa act gat gtc gca ggg ttc tcc cag cgc tac cac ctg gca	499
Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln Arg Tyr His Leu Ala	
120 125 130	
ccg ttg gcc act gca agc tgg gaa tgg atc aag acg gtc cac aac atg	547
Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys Thr Val His Asn Met	
135 140 145	
tgc cag cgc acc ctt gct ccc tca tcc atg agc att gac gag ctg cgt	595
Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser Ile Asp Glu Leu Arg	
150 155 160 165	
gac cac gga att aat gat att ttc cac tgg gct cgg ggc gtg gac tcc	643
Asp His Gly Ile Asn Asp Ile Phe His Trp Ala Arg Gly Val Asp Ser	
170 175 180	
aag cgt ttc cac cct gga aag cgt tcc gta gcg cta cgt aag tct tgg	691
Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala Leu Arg Lys Ser Trp	
185 190 195	
gat cca agt gga gca aag aag atc gtt ggt ttc gtt ggg cgc ctt gca	739
Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe Val Gly Arg Leu Ala	
200 205 210	
tcc gaa aag ggc gtg gag cgc ctt gct gga tta tcc gga cgc tca gac	787
Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu Ser Gly Arg Ser Asp	
215 220 225	
atc caa ttg gtc atc gtc ggt gat ggc cca gag gcc aag tac ctg cag	835
Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu Ala Lys Tyr Leu Gln	
230 235 240 245	
gaa atg atg ccg gat gcg atc ttc aca gga gct ctc gcc gcc gag gaa	883
Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala Leu Gly Gly Glu Glu	
250 255 260	
cta gcc acc acc tac gca tca ctc gat ctg ttt gtg cac cca ggt gag	931
Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe Val His Pro Gly Glu	
265 270 275	
ttt gaa acc ttc tgc cag gcg atc cag gaa gcc caa gca tca ggt gtg	979
Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala Gln Ala Ser Gly Val	
280 285 290	
ccc acc att ggc cca cgc gca ggt ggt ccc att gat ttg atc aac gaa	1027
Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile Asp Leu Ile Asn Glu	
295 300 305	
ggc gtc aac ggc ctg ctt ctt gat gtt gta gat ttc aag gaa acc ctc	1075
Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp Phe Lys Glu Thr Leu	
310 315 320 325	
ccc gct gca gcc gaa tgg att ttg gac gat tcc cgc cac tcc gaa atg	1123
Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser Arg His Ser Glu Met	
330 335 340	
tgc gca gct gct tgg gaa ggt gtg aaa gac aag acc tgg gaa gct ttg	1171
Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys Thr Trp Glu Ala Leu	
345 350 355	

tgc acc cag ctt ctc cag cac tac gcg gat gta atc gca ttg tca cag 1219  
 Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val Ile Ala Leu Ser Gln  
 360 365 370

cgc atc cca ctg aca ttc ttt ggc cct agc gct gaa gta gca aag ctt 1267  
 Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala Glu Val Ala Lys Leu  
 375 380 385

cca ctg tgg gtt gct cgc gcg ctg ggt gtt cgc acc cgc atc agc atc 1315  
 Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg Thr Arg Ile Ser Ile  
 390 395 400 405

gag gct taactctgca gaattaatcc atg 1344  
 Glu Ala

<210> 48

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met Arg Val Ala Ile Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly  
 1 5 10 15

Val Thr Asn Ser Val Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly  
 20 25 30

His Asp Ala Leu Val Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu  
 35 40 45

Ile Gly His Tyr Leu Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg  
 50 55 60

Val Pro Leu Ile Asp Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val  
 65 70 75 80

Thr Ser Val Leu Arg Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser  
 85 90 95

Pro Phe Val Leu Gly Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg  
 100 105 110

Ile Pro Ala Ile Ala Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln  
 115 120 125

Arg Tyr His Leu Ala Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys  
 130 135 140

Thr Val His Asn Met Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser  
 145 150 155 160

Ile Asp Glu Leu Arg Asp His Gly Ile Asn Asp Ile Phe His Trp Ala  
 165 170 175

Arg Gly Val Asp Ser Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala  
 180 185 190

Leu Arg Lys Ser Trp Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe  
 195 200 205

Val Gly Arg Leu Ala Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu  
210 215 220

Ser Gly Arg Ser Asp Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu  
225 230 235 240

Ala Lys Tyr Leu Gln Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala  
245 250 255

Leu Gly Gly Glu Glu Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe  
260 265 270

Val His Pro Gly Glu Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala  
275 280 285

Gln Ala Ser Gly Val Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile  
290 295 300

Asp Leu Ile Asn Glu Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp  
305 310 315 320

Phe Lys Glu Thr Leu Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser  
325 330 335

Arg His Ser Glu Met Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys  
340 345 350

Thr Trp Glu Ala Leu Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val  
355 360 365

Ile Ala Leu Ser Gln Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala  
370 375 380

Glu Val Ala Lys Leu Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg  
385 390 395 400

Thr Arg Ile Ser Ile Glu Ala  
405

<210> 49

<211> 1377

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1354)

<223> RXA02491

<400> 49

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agacgtcccg ctgctttctt cggcgatcta gaatgtgggc atg cgc gta gct atg 115  
Met Arg Val Ala Met  
1 5

att tcc atg cac acc tct cca ttg cag cag ccc gga act ggt gat tca 163  
Ile Ser Met His Thr Ser Pro Leu Gln Gln Pro Gly Thr Gly Asp Ser  
10 15 20



ggc ggc atg aac gtc tac att ctt tcg acc gcg act gag cta gcg aaa	211
Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala Thr Glu Leu Ala Lys	
25 30 35	
cag ggt atc gag gtc gat att tac act cgt gcc acg agg cct tct cag	259
Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala Thr Arg Pro Ser Gln	
40 45 50	
ggt gag atc gtg aga gta gct gag aat ttg cgg gtc att aat atc gct	307
Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg Val Ile Asn Ile Ala	
55 60 65	
gcg ggg ccg tat gag ggg ctt tcc aaa gag gag ctt cct act cag ttg	355
Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu Leu Pro Thr Gln Leu	
70 75 80 85	
gcg gcg ttt acc ggc gga atg ttg tcg ttt acg cgc cgg gag aag gtt	403
Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr Arg Arg Glu Lys Val	
90 95 100	
act tat gat ctg atc cat tct cac tat tgg ctg tct ggt cag gtg ggg	451
Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu Ser Gly Gln Val Gly	
105 110 115	
tgg ttg ctg cgc gat ttg tgg cgg att ccc ctt att cat acg gca cac	499
Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu Ile His Thr Ala His	
120 125 130	
act ttg gcg gcg gtg aag aat tct tat cgg gat gat tcg gac act ccg	547
Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp Asp Ser Asp Thr Pro	
135 140 145	
gag tcg gag gcg cgt cgc att tgt gag cag cag ctg gtg gat aac gct	595
Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln Leu Val Asp Asn Ala	
150 155 160 165	
gac gtg ttg gcg gtg aac act cag gag gag atg cag gat ttg atg cat	643
Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met Gln Asp Leu Met His	
170 175 180	
cac tac gat gcg gat ccg gat cgg att tct gtg gtg tca ccg ggt gcg	691
His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val Val Ser Pro Gly Ala	
185 190 195	
gac gtg gaa ctt tat agc cct gga aat gat cgc gcg acg gaa cgt tcc	739
Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg Ala Thr Glu Arg Ser	
200 205 210	
cgt cgt gag ctg ggc att ccg ctg cac aca aag gta gtg gct ttt gtg	787
Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys Val Val Ala Phe Val	
215 220 225	
ggt cgg ttg cag ccg ttt aag ggc ccg cag gtg ctg atc aag gcg gtt	835
Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val Leu Ile Lys Ala Val	
230 235 240 245	
gcg gcg ttg ttt gat cgc gat ccg gac cga aat ctg cgc gtc att att	883
Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn Leu Arg Val Ile Ile	
250 255 260	

tgt ggc ggc cct tct ggt ccg aat gcg aca ccg gat acc tat agg cat	931
Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro Asp Thr Tyr Arg His	
265 270 275	
atg gca gag gaa ctg ggc gtc gaa aag cga att cgc ttt ttg gac ccg	979
Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile Arg Phe Leu Asp Pro	
280 285 290	
cgc ccg ccg agc gag cta gtg gcc gtg tat cgg gcg gcg gac atc gtg	1027
Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg Ala Ala Asp Ile Val	
295 300 305	
gcc gtg cca agt ttt aat gag tcc ttc gga ctc gtc gcc atg gag gcg	1075
Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu Val Ala Met Glu Ala	
310 315 320 325	
caa gcc agc ggc aca ccg gtc att gcg gcc ccg gtt ggc ggc ctg ccc	1123
Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg Val Gly Gly Leu Pro	
330 335 340	
atc gca gtc gcg gaa ggg gag acg gga ttg ctt gtc gac ggc cac tcc	1171
Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu Val Asp Gly His Ser	
345 350 355	
ccg cat gcc tgg gcc gac gcc tta gcc aca ctc ttg gac gat gac gaa	1219
Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu Leu Asp Asp Asp Glu	
360 365 370	
acg cgc atc aga atg ggt gaa gac gcc gtc gaa cac gcc aga aca ttc	1267
Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu His Ala Arg Thr Phe	
375 380 385	
tcc tgg gcg gcc acc gcc gca cag cta tcg tcg ctg tac aac gac gct	1315
Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser Leu Tyr Asn Asp Ala	
390 395 400 405	
att gcc aac gaa aat gtc gac ggt gaa acg cat cac ggc taagtaaacg	1364
Ile Ala Asn Glu Asn Val Asp Gly Glu Thr His His Gly	
410 415	
cgcgctcgtgg aac	1377

&lt;210&gt; 50

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 50

Met Arg Val Ala Met Ile Ser Met His Thr Ser Pro Leu Gln Gln Pro
1 5 10 15

Gly Thr Gly Asp Ser Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala
20 25 30

Thr Glu Leu Ala Lys Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala
35 40 45

Thr Arg Pro Ser Gln Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg
50 55 60

Val Ile Asn Ile Ala Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu  
 65 70 75 80  
 Leu Pro Thr Gln Leu Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr  
 85 90 95  
 Arg Arg Glu Lys Val Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu  
 100 105 110  
 Ser Gly Gln Val Gly Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu  
 115 120 125  
 Ile His Thr Ala His Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp  
 130 135 140  
 Asp Ser Asp Thr Pro Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln  
 145 150 155 160  
 Leu Val Asp Asn Ala Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met  
 165 170 175  
 Gln Asp Leu Met His His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val  
 180 185 190  
 Val Ser Pro Gly Ala Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg  
 195 200 205  
 Ala Thr Glu Arg Ser Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys  
 210 215 220  
 Val Val Ala Phe Val Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val  
 225 230 235 240  
 Leu Ile Lys Ala Val Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn  
 245 250 255  
 Leu Arg Val Ile Ile Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro  
 260 265 270  
 Asp Thr Tyr Arg His Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile  
 275 280 285  
 Arg Phe Leu Asp Pro Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg  
 290 295 300  
 Ala Ala Asp Ile Val Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu  
 305 310 315 320  
 Val Ala Met Glu Ala Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg  
 325 330 335  
 Val Gly Gly Leu Pro Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu  
 340 345 350  
 Val Asp Gly His Ser Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu  
 355 360 365  
 Leu Asp Asp Asp Glu Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu  
 370 375 380  
 His Ala Arg Thr Phe Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser

His Gly

<400> 51																	
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ttcgcggatt tgtgcggggg agtgggtggg agagaaaacg																	115
Val Ile Val Val Ala																	5
1																	
atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct																	163
Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro																	20
10 15																	
atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt																	211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly																	35
25 30																	
ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat																	259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp																	50
40 45																	
cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca																	307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro																	65
55 60																	
cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag																	355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys																	85
70 75 80																	
ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg																	403
Phe Ser Val Tyr Pro Lys Ala Trp Val Val Ala Met Met Leu Gly Arg Val																	100
90 95																	
ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat																	451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn																	115
105 110																	
ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg																	499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu																	130
120 125																	
ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg																	547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val																	145
135 140																	

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct	595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala	
150 155 160 165	
tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag	643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu	
170 175 180	
ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat	691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn	
185 190 195	
ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc	739
Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly	
200 205 210	
cag cat gcg gtg acg ttg tgc cgc ctg gtt ccg cac aag cag att gag	787
Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu	
215 220 225	
cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta	835
His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val	
230 235 240 245	
gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg	883
Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr	
250 255 260	
ctg ggt gtg agc gat cgc gtg gtt ttc cac ggc cag gtc gcc gag gat	931
Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp	
265 270 275	
cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg cct tgc	979
His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser	
280 285 290	
cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc	1027
Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly	
295 300 305	
gtt ccg acg atc ggt tac cga agc tca ggc ggc ctg cgc gat tcc gtc	1075
Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val	
310 315 320 325	
gtc gac ggc gaa acc ggc ctg ctt gtc gac tcc aag gcc gag ctt att	1123
Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile	
330 335 340	
tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc	1171
Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu	
345 350 355	
ggc gcc agc gcg aag cag cgc gcc gaa aac tac aag tgg gac acc gcg	1219
Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala	
360 365 370	
gga gcg cag ttc gag gaa cta ctt ctt ggt ctt gcg tgc aaa aag	1264
Gly Ala Gln Phe Glu Glu Leu Leu Gly Leu Ala Ser Lys Lys	
375 380 385	

tagtcccagc ggcaacgccca tcc

1287

&lt;210&gt; 52

&lt;211&gt; 388

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 52

Val Ile Val Val Ala Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala  
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Arg Leu Asn Asn Pro Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr  
 20 25 30

Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly  
 35 40 45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly  
 50 55 60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser  
 65 70 75 80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met  
 85 90 95

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val  
 100 105 110

Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly  
 115 120 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro  
 130 135 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln  
 145 150 155 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu  
 165 170 175

Pro Ser Ala Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile  
 180 185 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys  
 195 200 205

Leu Asp Arg Asp Gly Gln His Ala Val Thr Leu Ser Arg Leu Val Pro  
 210 215 220

His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly  
 225 230 235 240

Val Val Leu Asp Val Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val  
 245 250 255

Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly  
 260 265 270

Gln Val Ala Glu Asp His Lys His Ala Leu Leu Glu Arg Ala Thr Ile

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<211> 751
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(751)
<223> FRXA02595
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ttcgcggatt	tgtgcggggg	agtgggtggg	agagaaaacg	gtg	atc	gtt	gtg	gcc									115
				Val	Ile	Val	Val	Ala									
				1				5									
atg	gct	tcc	att	atg	gct	tgt	tta	aaa	gca	gct	aga	ctg	aat	aac	cct		163
Met	Ala	Ser	Ile	Met	Ala	Cys	Leu	Lys	Ala	Ala	Arg	Leu	Asn	Asn	Pro		
				10				15						20			
atg	aag	atc	ctt	ttg	ttg	tgc	tgg	cgt	gat	acc	act	cat	cct	caa	ggg		211
Met	Lys	Ile	Leu	Leu	Leu	Cys	Trp	Arg	Asp	Thr	Thr	His	Pro	Gln	Gly		
			25					30					35				
ggc	gga	agt	gaa	cgc	tat	ctg	gag	cgg	gtg	ggg	gag	ttt	ttg	gcg	gat		259
Gly	Gly	Ser	Glu	Arg	Tyr	Leu	Glu	Arg	Val	Gly	Glu	Phe	Leu	Ala	Asp		
		40					45					50					
cag	ggc	cat	gag	gtg	gtg	ttt	cgt	act	gct	ggg	cac	acg	gat	gcg	cca		307
Gln	Gly	His	Glu	Val	Val	Phe	Arg	Thr	Ala	Gly	His	Thr	Asp	Ala	Pro		
		55				60					65						
cgg	cgt	tct	ttc	cgc	gat	ggg	gtg	agg	tat	tcc	agg	agc	ggg	ggg	aag		355
Arg	Arg	Ser	Phe	Arg	Asp	Gly	Val	Arg	Tyr	Ser	Arg	Ser	Gly	Gly	Lys		
70					75				80						85		

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 Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val  
 90 95 100  
 ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451  
 Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn  
 105 110 115  
 ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499  
 Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu  
 120 125 130  
 ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547  
 Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val  
 135 140 145  
 ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595  
 Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala  
 150 155 160 165  
 tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643  
 Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu  
 170 175 180  
 ctc att gcg ttg ggt gtg gat cag cag ccg att cat atc gtg cgc aat 691  
 Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn  
 185 190 195  
 ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc 739  
 Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly  
 200 205 210  
 cag cat gcg gtg 751  
 Gln His Ala Val  
 215

<210> 54  
 <211> 217  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 54  
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 Arg Leu Asn Asn Pro Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr  
 20 25 30  
 Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly  
 35 40 45  
 Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly  
 50 55 60  
 His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser  
 65 70 75 80  
 Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met  
 85 90 95



Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val  
 100 105 110

Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly  
 115 120 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro  
 130 135 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln  
 145 150 155 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu  
 165 170 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile  
 180 185 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys  
 195 200 205

Leu Asp Arg Asp Gly Gln His Ala Val  
 210 215

<210> 55  
 <211> 834  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(811)  
 <223> RXA02616

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cttcgaaaag ttttgtggca agaatcgga gcaggcgaaa ttg cag aag cac act 115  
 Leu Gln Lys His Thr  
 1 5

cga ggt ggc aag cac cgc aag cag act acc tcc cca gta act aag ggt 163  
 Arg Gly Gly Lys His Arg Lys Gln Thr Thr Ser Pro Val Thr Lys Gly  
 10 15 20

ggt gtc gct ttt gtt gca gta gct acc ggt gcc gtg tca act gca ggc 211  
 Gly Val Ala Phe Val Ala Val Ala Thr Gly Ala Val Ser Thr Ala Gly  
 25 30 35

gca ggc gga gca gtt gct gca cag gct tcc aat cag ccc gtt gag gtc 259  
 Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn Gln Pro Val Glu Val  
 40 45 50

aac ttc gag ctt act gca aac gac aca act gac ctc gtg gct gga agc 307  
 Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp Leu Val Ala Gly Ser  
 55 60 65

tcc gcc cct cag atc ctg tcc atc gct gag ttc aag cca gtt gtg aac 355  
 Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe Lys Pro Val Val Asn  
 70 75 80 85

ttg ggc gat cag atc gtt aag acc att cag tac aac gct gac cgc att 403  
 Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr Asn Ala Asp Arg Ile  
                     90                    95                    100

cag gct gac ctg gac gct cgt ggc cct tca gtg gtt cgc cct gct gaa 451  
 Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val Val Arg Pro Ala Glu  
                     105                    110                    115

ggt tct tac acc tcc ggc ttc ggt gct cgt tgg ggc acc aac cac aac 499  
 Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp Gly Thr Asn His Asn  
                     120                    125                    130

ggt gtg gat atc gct aac gca atc ggc act cca atc ctc gct gcc atg 547  
 Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro Ile Leu Ala Ala Met  
                     135                    140                    145

gac ggc act gtt atc gat gca ggt cct gct tcc ggt ttc ggt aac tgg 595  
 Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser Gly Phe Gly Asn Trp  
                     150                    155                    160                    165

gtt cgc ctc cag cac gaa gat ggc acc atc acc gtg tac ggc cac atg 643  
 Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr Val Tyr Gly His Met  
                     170                    175                    180

gaa acc gtt gag gtg acc gtt ggt cag act gtt aag gct ggc gag cgc 691  
 Glu Thr Val Glu Val Thr Val Gly Gln Thr Val Lys Ala Gly Glu Arg  
                     185                    190                    195

atc gca ggc atg ggt agc cga gga ttc tcc acc ggc tcc cac ctc cac 739  
 Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr Gly Ser His Leu His  
                     200                    205                    210

ttc gag gtt tac cct gca ggc ggt ggc gct gtt gat cca gct cct tgg 787  
 Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val Asp Pro Ala Pro Trp  
                     215                    220                    225

ctt gca gag cgc ggc att act ctt taattaactt ttgggcgacc ctt 834  
 Leu Ala Glu Arg Gly Ile Thr Leu  
                     230                    235

<210> 56  
 <211> 237  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 56  
 Leu Gln Lys His Thr Arg Gly Gly Lys His Arg Lys Gln Thr Thr Ser  
   1                    5                    10                    15

Pro Val Thr Lys Gly Gly Val Ala Phe Val Ala Val Ala Thr Gly Ala  
                     20                    25                    30

Val Ser Thr Ala Gly Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn  
                     35                    40                    45

Gln Pro Val Glu Val Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp  
                     50                    55                    60

Leu Val Ala Gly Ser Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe

65	70	75	80
Lys Pro Val Val Asn Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr	85	90	95
Asn Ala Asp Arg Ile Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val	100	105	110
Val Arg Pro Ala Glu Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp	115	120	125
Gly Thr Asn His Asn Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro	130	135	140
Ile Leu Ala Ala Met Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser	145	150	155
Gly Phe Gly Asn Trp Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr	165	170	175
Val Tyr Gly His Met Glu Thr Val Glu Val Thr Val Gly Gln Thr Val	180	185	190
Lys Ala Gly Glu Arg Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr	195	200	205
Gly Ser His Leu His Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val	210	215	220
Asp Pro Ala Pro Trp Leu Ala Glu Arg Gly Ile Thr Leu	225	230	235

&lt;210&gt; 57

&lt;211&gt; 866

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(843)

&lt;223&gt; RXA02627

&lt;400&gt; 57

gat gtc act gtg gaa agc caa cca gaa cgc gtc gtt gcc ctg ggt tgg	48
Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp	
1 5 10 15	
gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca	96
Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala	
20 25 30	
tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag	144
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu	
35 40 45	
gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg	192
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro	
50 55 60	
gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg	240

Glu	Tyr	Glu	Lys	Ile	Ala	Ala	Leu	Glu	Pro	Asp	Leu	Ile	Leu	Asp	Val		
65					70					75					80		
cgc	agc	tct	ggc	gac	cag	gaa	cgc	tat	gac	aag	ttg	tct	tca	atc	gca	288	
Arg	Ser	Ser	Gly	Asp	Gln	Glu	Arg	Tyr	Asp	Lys	Leu	Ser	Ser	Ile	Ala		
			85					90						95			
ctg	acc	atc	ggc	gtt	cca	gaa	ggc	gat	agc	tac	ctc	acc	cca	cgc	336		
Leu	Thr	Ile	Gly	Val	Pro	Glu	Gly	Gly	Asp	Ser	Tyr	Leu	Thr	Pro	Arg		
			100					105					110				
gct	gag	cag	gta	acc	atg	atc	gcc	act	gct	ctg	ggg	cag	gct	gaa	cgt	384	
Ala	Glu	Gln	Val	Thr	Met	Ile	Ala	Thr	Ala	Leu	Gly	Gln	Ala	Glu	Arg		
			115				120					125					
ggc	gaa	gaa	gtg	aac	gct	gaa	tac	gag	cag	ctc	act	gct	gat	att	cgt	432	
Gly	Glu	Glu	Val	Asn	Ala	Glu	Tyr	Glu	Gln	Leu	Thr	Ala	Asp	Ile	Arg		
			130			135					140						
gca	gct	cac	ccg	ggc	tgg	cct	gag	aag	acc	gcg	gct	gct	gta	tct	gca	480	
Ala	Ala	His	Pro	Gly	Trp	Pro	Glu	Lys	Thr	Ala	Ala	Ala	Val	Ser	Ala		
145					150				155						160		
acg	gca	acc	agc	tgg	ggc	gca	tac	atc	aag	ggc	tcc	aac	cgt	gta	gat	528	
Thr	Ala	Thr	Ser	Trp	Gly	Ala	Tyr	Ile	Lys	Gly	Ser	Asn	Arg	Val	Asp		
				165					170					175			
act	ttg	ctg	gac	ctg	ggc	ttc	cag	gaa	aac	cct	gag	ctg	gct	aaa	cag	576	
Thr	Leu	Leu	Asp	Leu	Gly	Phe	Gln	Glu	Asn	Pro	Glu	Leu	Ala	Lys	Gln		
			180				185						190				
caa	cct	ggc	gat	acg	ggc	ttc	tcc	atc	aaa	ttc	agt	gaa	gag	act	ttc	624	
Gln	Pro	Gly	Asp	Thr	Gly	Phe	Ser	Ile	Lys	Phe	Ser	Glu	Glu	Thr	Phe		
			195				200					205					
ggc	gtt	gtg	gat	tcc	gac	ctg	gtt	gtc	ggc	ttt	gcc	atc	ggc	atg	act	672	
Gly	Val	Val	Asp	Ser	Asp	Leu	Val	Val	Gly	Phe	Ala	Ile	Gly	Met	Thr		
			210			215					220						
cct	gag	gaa	atg	gca	gag	cag	gtt	cca	tgg	cag	atg	ttg	acc	gcc	act	720	
Pro	Glu	Glu	Met	Ala	Glu	Gln	Val	Pro	Trp	Gln	Met	Leu	Thr	Ala	Thr		
225					230					235					240		
cgt	gac	ggc	cgt	tcc	ttt	gtg	atg	ccc	cgt	gag	att	tcc	aat	gcg	ttt	768	
Arg	Asp	Gly	Arg	Ser	Phe	Val	Met	Pro	Arg	Glu	Ile	Ser	Asn	Ala	Phe		
				245					250					255			
tct	ttg	ggc	tcc	ccg	cag	tcc	act	cgg	ttc	gcg	tta	gac	gcc	ttg	gtg	816	
Ser	Leu	Gly	Ser	Pro	Gln	Ser	Thr	Arg	Phe	Ala	Leu	Asp	Ala	Leu	Val		
			260					265					270				
cca	ctt	ctg	gag	gag	cat	gca	ggg	gag	tagtggtccg	gtgggtgcggg	cag					866	
Pro	Leu	Leu	Glu	Glu	His	Ala	Gly	Glu									
			275				280										

&lt;210&gt; 58

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 58

Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp  
 1 5 10 15  
 Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala  
 20 25 30  
 Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu  
 35 40 45  
 Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro  
 50 55 60  
 Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val  
 65 70 75 80  
 Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala  
 85 90 95  
 Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg  
 100 105 110  
 Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg  
 115 120 125  
 Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg  
 130 135 140  
 Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala  
 145 150 155 160  
 Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp  
 165 170 175  
 Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln  
 180 185 190  
 Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe  
 195 200 205  
 Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr  
 210 215 220  
 Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr  
 225 230 235 240  
 Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe  
 245 250 255  
 Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val  
 260 265 270  
 Pro Leu Leu Glu Glu His Ala Gly Glu  
 275 280

&lt;210&gt; 59

&lt;211&gt; 702

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<223> RXA02650

gaatttttgc tgcaactgtg taaaaaccag cgctgaatta aagatcacct ttcaccctta 60

ccgacaaaagc aga 702

<210> 60  
 <211> 193  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 60  
 Met Val Asn Val Thr Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met  
     1                    5                    10                    15  
 Ser Lys Lys Glu Lys Arg Thr Thr Val Lys Gln Val Val Ala Leu Met  
           20                    25                    30  
 Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln  
           35                    40                    45  
 Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly  
           50                    55                    60  
 Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser  
           65                    70                    75                    80  
 Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser  
                     85                    90                    95  
 Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp  
           100                    105                    110  
 Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val  
           115                    120                    125  
 Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val  
           130                    135                    140  
 Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala  
           145                    150                    155                    160  
 Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu  
                     165                    170                    175  
 Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu  
           180                    185                    190  
 Ala

<210> 61  
 <211> 1071  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1048)  
 <223> RXA01094

<400> 61  
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cttgctgcct gactgttagg tttacgttgt tgtggatgtc	atg act ttg gcc acg	115
	Met Thr Leu Ala Thr	
	1 5	
att ccc tca cca ccg cag ggt gtg tgg tac ttg ggt ccc att ccg att	163	
Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu Gly Pro Ile Pro Ile		
	10 15 20	
agg gcc tat gcg atg tgc atc atc gct ggc att att gtt gcc att tgg	211	
Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile Ile Val Ala Ile Trp		
	25 30 35	
ctg acg aga aag cgc tac gcc gcc cgc ggt gga aac cct gaa atc gtc	259	
Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly Asn Pro Glu Ile Val		
	40 45 50	
ctt gat gca gcg atc gtg gca gtt cct gcc gga atc atc ggt gga cgc	307	
Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly Ile Ile Gly Gly Arg		
	55 60 65	
att tat cac gtc att acc gac aac caa aag tac ttc tgc gat acc tgt	355	
Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr Phe Cys Asp Thr Cys		
	70 75 80 85	
aac ccc gtc gac gcc ttc aaa atc acc aac ggt ggt ctg ggc atc tgg	403	
Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly Gly Leu Gly Ile Trp		
	90 95 100	
ggt gca gtg atc ctc ggt ggc ctg gca gtg gcc gta ttc ttc cgg tac	451	
Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala Val Phe Phe Arg Tyr		
	105 110 115	
aaa aag ctt cct ctt gca cct ttc gca gat gcc gtg gca cct gca gtt	499	
Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala Val Ala Pro Ala Val		
	120 125 130	
atc ctg gcg cag gga att ggt cgt ctg ggc aac tgg ttt aac cag gag	547	
Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn Trp Phe Asn Gln Glu		
	135 140 145	
ctc tac ggt gca gaa act acc gtt cca tgg gct ttg gaa atc tac tat	595	
Leu Tyr Gly Ala Glu Thr Val Pro Trp Ala Leu Glu Ile Tyr Tyr		
	150 155 160 165	
cgg gta gat gaa aat gga aaa ttc gca ccg gtg aca gga aca tcc acc	643	
Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val Thr Gly Thr Ser Thr		
	170 175 180	
ggt gaa gta atg gct act gtt cat cca aca ttc ctc tat gaa ctg ttg	691	
Gly Glu Val Met Ala Thr Val His Pro Thr Phe Leu Tyr Glu Leu Leu		
	185 190 195	
tgg aac cta ctg atc ttc gct ttg ttg atg tgg gct gac aag cga ttc	739	
Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp Ala Asp Lys Arg Phe		
	200 205 210	
aag ctg gaa cat ggc cga gta ttt gct ctc tac gta gct ggt tac acc	787	
Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr Val Ala Gly Tyr Thr		
	215 220 225	
ttg ggc cgt ttc tgg att gaa caa atg cgc gtt gat gaa gcc acg ctt	835	



Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val Asp Glu Ala Thr Leu  
 230 235 240 245  
 att ggc ggc atc cga atc aac acc atc gtc tcc gca gta gtg ttt gcc 883  
 Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser Ala Val Val Phe Ala  
 250 255 260  
 ggc gcg atc atc gtg ttc ttc ctg ttg aag aag ggt agg gaa act ccc 931  
 Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys Gly Arg Glu Thr Pro  
 265 270 275  
 gaa gag gta gat ccg act ttc gca gcg tct gtt gca gca gat gct gta 979  
 Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val Ala Ala Asp Ala Val  
 280 285 290  
 gct tcg cca gat aga aaa ccc ttg ccg aaa gca ggg gag ggc att gat 1027  
 Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala Gly Glu Gly Ile Asp  
 295 300 305  
 gga gaa acg ccc tca acg cga taggtttcaa ccataggcct gac 1071  
 Gly Glu Thr Pro Ser Thr Arg  
 310 315

&lt;210&gt; 62

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 62

Met Thr Leu Ala Thr Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu  
 1 5 10 15  
 Gly Pro Ile Pro Ile Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile  
 20 25 30  
 Ile Val Ala Ile Trp Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly  
 35 40 45  
 Asn Pro Glu Ile Val Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly  
 50 55 60  
 Ile Ile Gly Gly Arg Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr  
 65 70 75 80  
 Phe Cys Asp Thr Cys Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly  
 85 90 95  
 Gly Leu Gly Ile Trp Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala  
 100 105 110  
 Val Phe Phe Arg Tyr Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala  
 115 120 125  
 Val Ala Pro Ala Val Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn  
 130 135 140  
 Trp Phe Asn Gln Glu Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala  
 145 150 155 160  
 Leu Glu Ile Tyr Tyr Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val

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<210> 63
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1183)
<223> RXN00934
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<400> 63																
ccaacccctg tggtttggtg atttggatcc ggagcgtctc aagcgcctcta gggagcagac															60	
aaatgttcac aaaccggtgg cattacagga ggacaattag															gtg cga att gga atg	115
															Val Arg Ile Gly Met	5
															1	
gtc tgc ccg tac tcc ttc gat gag ccg ggc ggt gtt caa gcg cat atc															163	
Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly Val Gln Ala His Ile															20	
															10	15
ctt gac tta gcg cga acc ttc att gcc caa ggc cat gag gtt cag gtg															211	
Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly His Glu Val Gln Val															35	
															25	30
ctt ggt ccg tgt agt gcg gat acg cag gtg ccc gat ttc gtg gtg cgc															259	
Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro Asp Phe Val Val Arg															50	
															40	45
ggt ggt ggc agc atc ccg att ccg tac aat ggc tcg gtt gcc cgc ttg															307	
Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly Ser Val Ala Arg Leu																

55	60	65	
agc ttt ggg ccg aaa atg ttc aag gcc gtg cgc acg ttc ctc cgc gaa			355
Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu			
70	75	80	85
ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt			403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe			
	90	95	100
tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac			451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr			
	105	110	115
cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg			499
His Ala Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val			
	120	125	130
ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa			547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu			
	135	140	145
atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg			595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu			
	150	155	160
atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc			643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile			
	170	175	180
gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag			691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu			
	185	190	195
tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat			739
Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp			
	200	205	210
cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc			787
Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val			
	215	220	225
gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca			835
Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala			
	230	235	240
atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa			883
Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu			
	250	255	260
agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc			931
Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val			
	265	270	275
gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc			979
Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala			
	280	285	290
gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta			1027
Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu			
	295	300	305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg 1075  
 Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr  
 310 315 320 325  
  
 ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac tgg tcg aca 1123  
 Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr  
 330 335 340  
  
 gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa 1171  
 Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala Ile Asp Lys  
 345 350 355  
  
 gtg agg ctt gga tgacccttgt ttacctcctc atc 1206  
 Val Arg Leu Gly  
 360

<210> 64  
 <211> 361  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 64  
 Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly  
 1 5 10 15  
  
 Val Gln Ala His Ile Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly  
 20 25 30  
  
 His Glu Val Gln Val Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro  
 35 40 45  
  
 Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly  
 50 55 60  
  
 Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg  
 65 70 75 80  
  
 Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro  
 85 90 95  
  
 Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro  
 100 105 110  
  
 Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys  
 115 120 125  
  
 Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly  
 130 135 140  
  
 Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly  
 145 150 155 160  
  
 Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys  
 165 170 175  
  
 Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu  
 180 185 190  
  
 Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala

195	200	205
Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly		
210	215	220
Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp		
225	230	235 240
Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro		
	245	250 255
Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala		
	260	265 270
Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val		
	275	280 285
Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly		
	290	295 300
Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro		
305	310	315 320
Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala		
	325	330 335
Tyr Asp Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr		
	340	345 350
Ile Ala Ile Asp Lys Val Arg Leu Gly		
	355	360

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(789)  
 <223> FRXA00934

<400> 65	
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Pro Ser Phe Ser Met Ala Ala Leu Pro Phe Ala Glu Gly Pro Ile Val	
1 5 10 15	
gct act tac cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc	96
Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe	
20 25 30	
tta cca gtg ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc	144
Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala	
35 40 45	
gtg tct gaa atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat	192
Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp	
50 55 60	
ccc gtg ctg atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg	240

Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala  
65 70 75 80

cgc caa atc gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc 288  
Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg  
85 90 95

ctc gat gag tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc 336  
Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr  
100 105 110

agg ctg gat cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg 384  
Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro  
115 120 125

cga gaa gtc gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa 432  
Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu  
130 135 140

aag gca gca atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc 480  
Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr  
145 150 155 160

ggc ggc gaa agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga 528  
Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly  
165 170 175

tgc gct gtc gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat 576  
Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp  
180 185 190

tct gaa gcc gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac 624  
Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp  
195 200 205

gcc gac cta gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc 672  
Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser  
210 215 220

cgt tcc acg ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac 720  
Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp  
225 230 235 240

tgg tcg aca gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg 768  
Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala  
245 250 255

atc gac aaa gtg agg ctt gga tgacccttgt ttacctcctc atc 812  
Ile Asp Lys Val Arg Leu Gly  
260

&lt;210&gt; 66

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 66

Pro Ser Phe Ser Met Ala Ala Leu Pro Phe Ala Glu Gly Pro Ile Val  
1 5 10 15

Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe  
                   20                                  25                                  30  
 Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala  
                   35                                  40                                  45  
 Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp  
                   50                                  55                                  60  
 Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala  
                   65                                  70                                  75                                  80  
 Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg  
                                   85                                  90                                  95  
 Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr  
                   100                                  105                                  110  
 Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro  
                   115                                  120                                  125  
 Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu  
                   130                                  135                                  140  
 Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr  
                   145                                  150                                  155                                  160  
 Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly  
                   165                                  170                                  175  
 Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp  
                   180                                  185                                  190  
 Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp  
                   195                                  200                                  205  
 Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser  
                   210                                  215                                  220  
 Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp  
                   225                                  230                                  235                                  240  
 Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala  
                   245                                  250                                  255  
 Ile Asp Lys Val Arg Leu Gly  
                   260

&lt;210&gt; 67

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXA02605

&lt;400&gt; 67

tccgatcctg tcatctacat gtgggagact ttccttaccc aggaattgcc tgcatacctt 60

gagcagaact tcggcggttgc gcgaaacaac aactccattg gtg gcc tgt cca tgg 115  
Val Ala Cys Pro Trp  
1 5

gcg gga act gcc gcg ctg aac ctc gca gca aag cac cca gat cag ttc 163  
Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys His Pro Asp Gln Phe  
10 15 20

cgc cag gct atg tct tgg tcc ggc tac ttg aac acc act gcg cca ggc 211  
Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn Thr Thr Ala Pro Gly  
25 30 35

atg caa acc ctg ctg cgt gtg gcc atg ctg gac acc ggt gga ttc aac 259  
Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp Thr Gly Gly Phe Asn  
40 45 50

gtc aac gca atg tat ggc tca atc att aac cca cgt cgt ttt gaa aac 307  
Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro Arg Arg Phe Glu Asn  
55 60 65

gac cca ttc tgg aac atg ggc ggc ttg gct aac acc gac gtc tac atc 355  
Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn Thr Asp Val Tyr Ile  
70 75 80 85

tct gca gct tcc ggc ctg tgg agc cct cag gat gat gga gtt cgc gta 403  
Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp Asp Gly Val Arg Val  
90 95 100

gac cac cgc ctc act ggt tct gtg ctt gaa ttc gtg gca atg aca tcc 451  
Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe Val Ala Met Thr Ser  
105 110 115

acc agg att tgg gaa gca aag gca agg ctt cag ggt ctg aac cca act 499  
Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln Gly Leu Asn Pro Thr  
120 125 130

gcg gat tac cca atg tat ggc att cac ggc tgg gct cag ttc aac tcc 547  
Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp Ala Gln Phe Asn Ser  
135 140 145

cag ctg gag aga act cag ggt cgt gtt cta gac gtc atg aac gcc tgg 595  
Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp Val Met Asn Ala Trp  
150 155 160 165

tagagccaca ccaaaggcca cac 618

&lt;210&gt; 68

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 68

Val Ala Cys Pro Trp Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys  
1 5 10 15

His Pro Asp Gln Phe Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn  
20 25 30

Thr Thr Ala Pro Gly Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp



35	40	45
Thr Gly Gly Phe Asn Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro		
50	55	60
Arg Arg Phe Glu Asn Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn		
65	70	75
Thr Asp Val Tyr Ile Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp		
	85	90
Asp Gly Val Arg Val Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe		
	100	105
Val Ala Met Thr Ser Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln		
	115	120
Gly Leu Asn Pro Thr Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp		
	130	135
Ala Gln Phe Asn Ser Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp		
	145	150
Val Met Asn Ala Trp		
	165	

<210> 69  
 <211> 1386  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1363)  
 <223> RXN00525

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tggttgacgg gcgcattcatt ggggtctgagg tgaacactc atg agc ctt gca gaa 115  
 Met Ser Leu Ala Glu  
 1 5

tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163  
 Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala  
 10 15 20

ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211  
 Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly  
 25 30 35

att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259  
 Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu  
 40 45 50

gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307  
 Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro  
 55 60 65

gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca 355

Asp	Glu	Asp	Ser	Pro	Glu	Pro	Asp	Met	Phe	Ala	Phe	Ser	Gly	Ala	Ala		
70					75					80					85		
aac	tct	agt	ggc	aat	ctg	att	ccg	gaa	gaa	aca	ggt	gat	acg	ctg	cgc		403
Asn	Ser	Ser	Gly	Asn	Leu	Ile	Pro	Glu	Glu	Thr	Val	Asp	Thr	Leu	Arg		
				90					95					100			
gat	cgt	ttc	gca	ggc	agc	atc	acg	gga	atc	agc	ggt	ggc	gga	atg	ggt		451
Asp	Arg	Phe	Ala	Gly	Ser	Ile	Thr	Gly	Ile	Ser	Val	Gly	Gly	Met	Gly		
			105					110					115				
acg	caa	ggc	act	ctc	atc	ggc	gac	acc	gca	gat	ctt	aaa	tcc	gat	ctc		499
Thr	Gln	Gly	Thr	Leu	Ile	Gly	Asp	Thr	Ala	Asp	Leu	Lys	Ser	Asp	Leu		
		120					125					130					
ctc	ggc	gtc	aac	gag	gat	tat	atg	tgg	atg	aat	ggc	gtc	gaa	atg	aac		547
Leu	Gly	Val	Asn	Glu	Asp	Tyr	Met	Trp	Met	Asn	Gly	Val	Glu	Met	Asn		
	135					140					145						
tac	ggc	cgc	gcc	atc	acg	caa	gac	gat	ggt	gcc	gct	cag	cgc	ccc	ggt		595
Tyr	Gly	Arg	Ala	Ile	Thr	Gln	Asp	Asp	Val	Ala	Ala	Gln	Arg	Pro	Val		
	150				155					160					165		
gcg	gtc	atc	gcc	cca	gac	acc	ttt	aat	acg	ctt	ttc	gac	gca	aac	ccc		643
Ala	Val	Ile	Ala	Pro	Asp	Thr	Phe	Asn	Thr	Leu	Phe	Asp	Ala	Asn	Pro		
				170					175					180			
aac	ctc	gct	ctg	ggg	tcc	gaa	gta	gct	ttt	gaa	ctc	aac	ggt	caa	gag		691
Asn	Leu	Ala	Leu	Gly	Ser	Glu	Val	Ala	Phe	Glu	Leu	Asn	Gly	Gln	Glu		
			185					190					195				
aca	ttt	ttg	cgg	ggt	atc	ggt	gtg	tat	aaa	gaa	gcc	gca	gca	ggt	gga		739
Thr	Phe	Leu	Arg	Val	Ile	Gly	Val	Tyr	Lys	Glu	Ala	Ala	Ala	Gly	Gly		
		200					205					210					
ctt	gtg	gga	agc	aat	cca	acc	gtc	cac	acc	tac	acc	cca	tat	acg	gtg		787
Leu	Val	Gly	Ser	Asn	Pro	Thr	Val	His	Thr	Tyr	Thr	Pro	Tyr	Thr	Val		
	215					220					225						
gcc	aat	gac	atc	acc	cac	acg	gaa	gat	gga	ttg	aac	acg	tta	agt	atc		835
Ala	Asn	Asp	Ile	Thr	His	Thr	Glu	Asp	Gly	Leu	Asn	Thr	Leu	Ser	Ile		
	230				235					240					245		
cgt	gca	gct	cag	ggc	gta	gac	cag	gat	tca	ctt	aag	ggt	tca	ctg	caa		883
Arg	Ala	Ala	Gln	Gly	Val	Asp	Gln	Asp	Ser	Leu	Lys	Gly	Ser	Leu	Gln		
				250				255						260			
acc	tac	ttc	gac	gcg	ctg	tac	gcc	aac	aat	gac	tgc	cac	cac	ggt	gcc		931
Thr	Tyr	Phe	Asp	Ala	Leu	Tyr	Ala	Asn	Asn	Asp	Ser	His	His	Val	Ala		
			265					270					275				
atg	ttg	gac	ttc	cgt	aaa	cag	atc	gaa	gag	ttc	aac	acc	att	ctc	ggc		979
Met	Leu	Asp	Phe	Arg	Lys	Gln	Ile	Glu	Glu	Phe	Asn	Thr	Ile	Leu	Gly		
		280					285					290					
gca	atg	agt	ttg	ggt	atc	tca	gcc	atc	ggc	gga	att	tcc	ttg	ctt	gtc		1027
Ala	Met	Ser	Leu	Gly	Ile	Ser	Ala	Ile	Gly	Gly	Ile	Ser	Leu	Leu	Val		
	295					300					305						
ggt	ggc	atc	gga	gtg	atg	aac	att	atg	ttg	gtg	tct	gtc	acc	gag	cga		1075
Gly	Gly	Ile	Gly	Val	Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg		

310	315	320	325	
acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac				1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp	330	335	340	
att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt				1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly	345	350	355	
ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg tcc				1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser	360	365	370	
agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc				1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile	375	380	385	
gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc				1315
Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro	390	395	400	405
gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag				1363
Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu	410	415	420	
taaaagcctc gtttttaagg tag				1386

<210> 70  
 <211> 421  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 70  
 Met Ser Leu Ala Glu Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser  
 1 5 10 15  
 Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile  
 20 25 30  
 Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln  
 35 40 45  
 Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln  
 50 55 60  
 Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala  
 65 70 75 80  
 Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr  
 85 90 95  
 Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser  
 100 105 110  
 Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp  
 115 120 125  
 Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn  
 130 135 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala  
 145 150 155 160  
 Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu  
 165 170 175  
 Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu  
 180 185 190  
 Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu  
 195 200 205  
 Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr  
 210 215 220  
 Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu  
 225 230 235 240  
 Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu  
 245 250 255  
 Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp  
 260 265 270  
 Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe  
 275 280 285  
 Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly  
 290 295 300  
 Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu Val  
 305 310 315 320  
 Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly  
 325 330 335  
 Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile  
 340 345 350  
 Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu  
 355 360 365  
 Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu  
 370 375 380  
 Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe  
 385 390 395 400  
 Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp  
 405 410 415  
 Ala Leu Arg Tyr Glu  
 420

&lt;210&gt; 71

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; FRXA00525

&lt;400&gt; 71

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				Met	Ser	Leu	Ala	Glu	
				1				5	

tca	att	ctt	ttg	gcg	ctc	acc	agc	ctg	aga	agc	aac	aag	atg	cgt	gca	163
Ser	Ile	Leu	Leu	Ala	Leu	Thr	Ser	Leu	Arg	Ser	Asn	Lys	Met	Arg	Ala	
				10				15						20		

ttg	ttg	acg	ctg	tta	gga	gtc	atc	att	ggg	atc	gca	tca	gtc	atc	gga	211
Leu	Leu	Thr	Leu	Leu	Gly	Val	Ile	Ile	Gly	Ile	Ala	Ser	Val	Ile	Gly	
				25				30					35			

att	ttg	acc	att	ggg	aaa	gcc	ctg	cag	gat	caa	act	ttg	aat	agt	ttg	259
Ile	Leu	Thr	Ile	Gly	Lys	Ala	Leu	Gln	Asp	Gln	Thr	Leu	Asn	Ser	Leu	
		40					45					50				

gaa	agc	ttg	ggc	gcg	aat	gat	ctg	tcg	gcg	cag	gtg	gag	gaa	cgc	ccc	307
Glu	Ser	Leu	Gly	Ala	Asn	Asp	Leu	Ser	Ala	Gln	Val	Glu	Glu	Arg	Pro	
	55					60					65					

gac	gaa	gat	tcc	ccc	gaa	ccc	gat	atg	ttc	gct	ttt	tct	ggg	gct	gca	355
Asp	Glu	Asp	Ser	Pro	Glu	Pro	Asp	Met	Phe	Ala	Phe	Ser	Gly	Ala	Ala	
	70				75				80					85		

aac	tct	agt	ggc	aat	ctg	att	ccg	gaa	gaa	aca	gtt	gat	acg	ctg	cgc	403
Asn	Ser	Ser	Gly	Asn	Leu	Ile	Pro	Glu	Glu	Thr	Val	Asp	Thr	Leu	Arg	
				90					95					100		

gat	cgt	ttc	gca	ggc	agc	atc	acg	gga	atc	agc	gtt	ggc	gga	atg	ggg	451
Asp	Arg	Phe	Ala	Gly	Ser	Ile	Thr	Gly	Ile	Ser	Val	Gly	Gly	Met	Gly	
		105						110				115				

acg	caa	ggc	act	ctc	atc	ggc	gac	acc	gca	gat	ctt	aaa	tcc	gat	ctc	499
Thr	Gln	Gly	Thr	Leu	Ile	Gly	Asp	Thr	Ala	Asp	Leu	Lys	Ser	Asp	Leu	
		120					125					130				

ctc	ggc	gtc	aac	gag	gat	tat	atg	tgg	atg	aat	ggc	gtc	gaa	atg	aac	547
Leu	Gly	Val	Asn	Glu	Asp	Tyr	Met	Trp	Met	Asn	Gly	Val	Glu	Met	Asn	
	135					140					145					

tac	ggc	cgc	gcc	atc	acg	caa	gac	gat	gtt	gcc	gct	cag	cgc	ccc	gtt	595
Tyr	Gly	Arg	Ala	Ile	Thr	Gln	Asp	Asp	Val	Ala	Ala	Gln	Arg	Pro	Val	
	150				155				160					165		

gcg	gtc	atc	gcc	cca	gac	acc	ttt	aat	acg	ctt	ttc	gac	gca	aac	ccc	643
Ala	Val	Ile	Ala	Pro	Asp	Thr	Phe	Asn	Thr	Leu	Phe	Asp	Ala	Asn	Pro	
			170						175					180		

aac	ctc	gct	ctg	ggg	tcc	gaa	gta	gct	ttt	gaa	ctc	aac	ggg	caa	gag	691
Asn	Leu	Ala	Leu	Gly	Ser	Glu	Val	Ala	Phe	Glu	Leu	Asn	Gly	Gln	Glu	
			185					190					195			

aca	ttt	ttg	cgg	gtt	atc	ggg	gtg	tat	aaa	gaa	gcc	gca	gca	ggg	gga	739
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Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly  
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ctt gtg gga agc aat cca acc  
 Leu Val Gly Ser Asn Pro Thr  
 215 220

760

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 <212> PRT  
 <213> Corynebacterium glutamicum

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Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile  
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Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln  
 35 40 45

Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln  
 50 55 60

Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala  
 65 70 75 80

Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr  
 85 90 95

Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser  
 100 105 110

Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp  
 115 120 125

Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn  
 130 135 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala  
 145 150 155 160

Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu  
 165 170 175

Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu  
 180 185 190

Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu  
 195 200 205

Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr  
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<210> 73  
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 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(594)

&lt;223&gt; FRXA00556

&lt;400&gt; 73

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Tyr Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Lys Asp Gly	
1 5 10 15	
ttg aac acg tta agt atc cgt gca gct cag ggc gta gac cag gat tca	96
Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser	
20 25 30	
ctt aag ggt tca ctg caa acc tac ttc gac gcg ctg tac gcc aac aat	144
Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn	
35 40 45	
gac tcg cac cac gtt gcc atg ttg gac ttc cgt aaa cag atc gaa gag	192
Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu	
50 55 60	
ttc aac acc att ctc ggc gca atg agt ttg ggt atc tca gcc atc ggc	240
Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly	
65 70 75 80	
gga att tcc ttg ctt gtc ggt ggc atc gga gtg atg aac att atg ttg	288
Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu	
85 90 95	
gtg tct gtc acc gag cga acc cgc gaa atc ggt gtc cga aaa gcc ctc	336
Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu	
100 105 110	
ggc gct cgt cga cgt gac att cgc ctg caa ttc gtc gtt gaa gcc atg	384
Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met	
115 120 125	
atc att tgt ttc atc ggt ggc atc ctc ggc gtg ctt ttg ggc ggc att	432
Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile	
130 135 140	
ttg gga ttg atc atg tcc agc gct att ggc tac att tcc ttg cca cca	480
Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro	
145 150 155 160	
ctg agt gga atc gtg atc gcc ttg gta ttt tcc atg gct atc ggc ctg	528
Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu	
165 170 175	
ttt ttc ggc tac tac ccc gcc aac aag gca gca aag ctc gat cca att	576
Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile	
180 185 190	
gac gcc ttg cgt tat gag taaaagcctc gtttttaagg tag	617
Asp Ala Leu Arg Tyr Glu	
195	

&lt;210&gt; 74

<211> 198  
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 <213> Corynebacterium glutamicum

<400> 74

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 Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn  
 35 40 45  
 Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu  
 50 55 60  
 Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly  
 65 70 75 80  
 Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu  
 85 90 95  
 Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu  
 100 105 110  
 Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met  
 115 120 125  
 Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile  
 130 135 140  
 Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro  
 145 150 155 160  
 Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu  
 165 170 175  
 Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile  
 180 185 190  
 Asp Ala Leu Arg Tyr Glu  
 195

<210> 75  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(916)  
 <223> RXA02750

<400> 75

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 Met Ala Val Leu Phe  
 1 5



tcc atc atg ggt gcg ctc atc ctt ttg gtc ctg tac gtg ctg ttt tta	163
Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu Tyr Val Leu Phe Leu	
10 15 20	
gga aaa ctg caa att gac ggt ctc atg gtg gat cta cct gac tca gcc	211
Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp Leu Pro Asp Ser Ala	
25 30 35	
cga gac gat gtt gaa gga ttc gtc ttc aat tgg gtg ttt tcc gga att	259
Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp Val Phe Ser Gly Ile	
40 45 50	
ctc atc acg tcc gca atc act gtt ccg caa gca gca ctt gga gtg ctg	307
Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala Ala Leu Gly Val Leu	
55 60 65	
gtt gaa gat cgc acc cgc gga ggc atc aaa gat ttc ctc gtg gca ccc	355
Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp Phe Leu Val Ala Pro	
70 75 80 85	
gta tcc aga acg acg ctg acg gtg tcc tat atc ttc gca gca gtc att	403
Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile Phe Ala Ala Val Ile	
90 95 100	
gtc gcc atg acg att ttg atc ttt gaa atc gtg gtg gga agt att ggt	451
Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val Val Gly Ser Ile Gly	
105 110 115	
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Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile Ala Arg Val Leu Glu	
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ttg gta gtc gcc ttg ctt ctg ctc acc ctg gtg ttt tcc gca att gca	547
Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val Phe Ser Ala Ile Ala	
135 140 145	
gca ttt ctg atc acc ttg gtg aaa tct caa ggc gga atg tct gcg ctt	595
Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly Gly Met Ser Ala Leu	
150 155 160 165	
tca agc ctg gta ggc acc ctg gcg ggc ttt tta tct gct gct tat att	643
Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu Ser Ala Ala Tyr Ile	
170 175 180	
cca ccc atc gca ttg cct gaa gca gtg aca aac gtg ttg aac ttc ctc	691
Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn Val Leu Asn Phe Leu	
185 190 195	
ccg ttt acc cca gct gga atg ttg atc aga caa att gtg gtt gcc cca	739
Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln Ile Val Val Ala Pro	
200 205 210	
gca ttg gac gcg att tca ctt cca ccc gaa gcc ttc gat atc ttc caa	787
Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala Phe Asp Ile Phe Gln	
215 220 225	
ttc gga tac gga ctc aaa ctg gaa atg ttt ggg gaa ccc gtt tct aca	835
Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly Glu Pro Val Ser Thr	
230 235 240 245	

tgg gtg gca gta gga att gtt gcc tca tgg gga gtg gtg ttt gga ctc 883  
 Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly Val Val Phe Gly Leu  
                   250                                  255                                  260

att gcc gcg ttc aaa atg aaa agc gtg gtg cga taaatcctgc taaagaatgc 936  
 Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg  
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ttc 939

<210> 76

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Tyr Val Leu Phe Leu Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp  
                   20                                  25                                  30

Leu Pro Asp Ser Ala Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp  
                   35                                  40                                  45

Val Phe Ser Gly Ile Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala  
   50                                  55                                  60

Ala Leu Gly Val Leu Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp  
   65                                  70                                  75                                  80

Phe Leu Val Ala Pro Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile  
                   85                                  90                                  95

Phe Ala Ala Val Ile Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val  
                   100                                  105                                  110

Val Gly Ser Ile Gly Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile  
                   115                                  120                                  125

Ala Arg Val Leu Glu Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val  
   130                                  135                                  140

Phe Ser Ala Ile Ala Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly  
 145                                  150                                  155                                  160

Gly Met Ser Ala Leu Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu  
                   165                                  170                                  175

Ser Ala Ala Tyr Ile Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn  
                   180                                  185                                  190

Val Leu Asn Phe Leu Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln  
                   195                                  200                                  205

Ile Val Val Ala Pro Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala  
   210                                  215                                  220

Phe Asp Ile Phe Gln Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly  
 225                                  230                                  235                                  240

Glu Pro Val Ser Thr Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly  
 245 250 255

Val Val Phe Gly Leu Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg  
 260 265 270

<210> 77

<211> 1815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1792)

<223> RXN02096

<400> 77

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 Met Gly Leu Asp Val  
 1 5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163  
 Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp  
 10 15 20

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 Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg  
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ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg 259  
 Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg  
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gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct 307  
 Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser  
 55 60 65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa 355  
 Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu  
 70 75 80 85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act 403  
 Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr  
 90 95 100

ttg gag ctc ggc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca 451  
 Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr  
 105 110 115

gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat 499  
 Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His  
 120 125 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc 547  
 Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu  
 135 140 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc	595
Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser	
150 155 160 165	
aca gaa aag cag tac aag att ctt gcg cct gcc cct ggt cga ggc cgt	643
Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg	
170 175 180	
ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg	691
Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala	
185 190 195	
ctg cca gca gca acg gaa gaa aca cga gtt gat gcc ggg agg cta cgc	739
Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg	
200 205 210	
acc agt acc tcc ggt ttc aaa ttg ctc agt tta ttc aag cag gtc cgt	787
Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg	
215 220 225	
tggt ctc gtc gtc gcg gtc atc gcg ttg ttg ctg gtg ggc gta gcc gcc	835
Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala	
230 235 240 245	
gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg	883
Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val	
250 255 260	
caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc	931
Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser	
265 270 275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc	979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile	
280 285 290	
acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca	1027
Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser	
295 300 305	
ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg	1075
Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met	
310 315 320 325	
tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg	1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser	
330 335 340	
tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg	1171
Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr	
345 350 355	
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca	1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala	
360 365 370	
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att	1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile	
375 380 385	
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc	1315

Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala  
 390 395 400 405  
 agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc 1363  
 Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr  
 410 415 420  
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 Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly  
 425 430 435  
 gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc 1459  
 Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile  
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 Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala  
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 Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser  
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 Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met Gly Leu Met Phe Gly  
 490 495 500  
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 Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser Tyr Gln Gln Ala Ala  
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 Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala Thr Gln Pro Ser Val  
 520 525 530  
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 Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg Leu Pro Arg Ser Leu  
 535 540 545  
 tat tgc ttg acg acg tca cct tcg gct att cag acg atc cga tcc 1792  
 Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln Thr Ile Arg Ser  
 550 555 560  
 tagacaacgt caccgtccag atc 1815

&lt;210&gt; 78

&lt;211&gt; 564

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78

Met Gly Leu Asp Val Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu  
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Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu  
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Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg  
 35 40 45

Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu  
 50 55 60  
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe  
 65 70 75 80  
 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala  
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 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu  
 100 105 110  
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His  
 115 120 125  
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp  
 130 135 140  
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu  
 145 150 155 160  
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala  
 165 170 175  
 Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu  
 180 185 190  
 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp  
 195 200 205  
 Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu  
 210 215 220  
 Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu  
 225 230 235 240  
 Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala  
 245 250 255  
 Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile  
 260 265 270  
 Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala  
 275 280 285  
 Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly  
 290 295 300  
 Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr  
 305 310 315 320  
 Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp  
 325 330 335  
 Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val  
 340 345 350  
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                                         Met Gly Leu Asp Val
                                         1                               5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
              10                               15                               20

ttt atc gat cgc ctt cca aac aaa tac gag qaa gtc att ggc qaa cgc 211

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Phe	Ile	Asp	Arg	Leu	Pro	Asn	Lys	Tyr	Glu	Glu	Val	Ile	Gly	Glu	Arg		
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ggc	ctg	acg	ctt	tct	ggt	ggt	caa	cgc	caa	cgc	atc	gcc	ctc	gca	cgg	259	
Gly	Leu	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Leu	Ala	Arg		
		40					45					50					
gct	ttc	ctg	gcg	cat	ccc	aaa	gtg	ttg	gtg	ctt	gat	gat	gcc	acc	tct	307	
Ala	Phe	Leu	Ala	His	Pro	Lys	Val	Leu	Val	Leu	Asp	Asp	Ala	Thr	Ser		
	55					60					65						
gcc	att	gat	gcc	tcc	act	gag	gac	cgc	att	ttc	cag	gcc	ttg	cgc	gaa	355	
Ala	Ile	Asp	Ala	Ser	Thr	Glu	Asp	Arg	Ile	Phe	Gln	Ala	Leu	Arg	Glu		
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gaa	ctg	cac	gat	gtc	acc	att	ttg	atc	atc	gcg	cac	cgc	cac	tcc	act	403	
Glu	Leu	His	Asp	Val	Thr	Ile	Leu	Ile	Ile	Ala	His	Arg	His	Ser	Thr		
				90					95					100			
ttg	gag	ctc	ggc	gat	cgg	gtt	ggt	ctg	gtc	gaa	gat	gga	cgg	gta	aca	451	
Leu	Glu	Leu	Gly	Asp	Arg	Val	Gly	Leu	Val	Glu	Asp	Gly	Arg	Val	Thr		
			105					110					115				
gca	ctg	gga	cgc	ttg	agt	gag	atg	cgt	gat	cac	gct	cgt	ttc	tcg	cat	499	
Ala	Leu	Gly	Pro	Leu	Ser	Glu	Met	Arg	Asp	His	Ala	Arg	Phe	Ser	His		
		120					125					130					
ctg	atg	gct	ctt	gat	ttc	cag	gat	tct	cac	gat	ccg	gaa	ttc	acc	ctc	547	
Leu	Met	Ala	Leu	Asp	Phe	Gln	Asp	Ser	His	Asp	Pro	Glu	Phe	Thr	Leu		
	135					140					145						
gac	aac	ggt	tca	cta	ccc	agc	caa	gag	caa	ttg	tgg	ccg	gag	gtc	tcc	595	
Asp	Asn	Gly	Ser	Leu	Pro	Ser	Gln	Glu	Gln	Leu	Trp	Pro	Glu	Val	Ser		
	150				155					160					165		
aca	gaa	aag	cag	tac	aag	att	ctt	gcg	cct	gcc	cct	ggt	cga	ggc	cgt	643	
Thr	Glu	Lys	Gln	Tyr	Lys	Ile	Leu	Ala	Pro	Ala	Pro	Gly	Arg	Gly	Arg		
				170					175					180			
ggc	atg	tcc	atg	cca	gca	acc	cct	gag	ctg	ctc	gcc	cag	att	gag	gcg	691	
Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Gln	Ile	Glu	Ala		
			185					190					195				
ctg	cca	gca	gca	acg	gaa	gaa	aca	cga	gtt	gat	gcc	ggg	agg	cta	cgc	739	
Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp	Ala	Gly	Arg	Leu	Arg		
		200					205					210					
acc	agt	acc	tcc	ggt	ttc	aaa	ttg	ctc	agt	tta	ttc	aag	cag	gtc	cgt	787	
Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	Phe	Lys	Gln	Val	Arg		
	215					220					225						
tgg	ctc	gtc	gtc	gcg	gtc	atc	gcg	ttg	ttg	ctg	gtg	ggc	gta	gcc	gcc	835	
Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	Val	Gly	Val	Ala	Ala		
	230				235					240					245		
gat	cta	gca	ttt	cca	aca	ctg	atg	cgc	gca	gcc	atc	gac	aac	ggt	gtg	883	
Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala	Ile	Asp	Asn	Gly	Val		
				250					255					260			
caa	gca	caa	agc	acc	tcc	acg	ttg	tgg	tgg	atc	gcc	atc	gca	ggc	agc	931	
Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile	Ala	Ile	Ala	Gly	Ser		



265	270	275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile 280 285 290			979
acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser 295 300 305			1027
ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met 310 315 320 325			1075
tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tog Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser 330 335 340			1123
tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr 345 350 355			1171
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala 360 365 370			1219
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile 375 380 385			1267
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala 390 395 400 405			1315
agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr 410 415 420			1363
gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly 425 430 435			1411
gaa gca Glu Ala			1417

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 80  
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 Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu  
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 Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg  
 35 40 45

Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu  
 50 55 60  
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe  
 65 70 75 80  
 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala  
 85 90 95  
 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu  
 100 105 110  
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His  
 115 120 125  
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp  
 130 135 140  
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu  
 145 150 155 160  
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala  
 165 170 175  
 Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu  
 180 185 190  
 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp  
 195 200 205  
 Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu  
 210 215 220  
 Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu  
 225 230 235 240  
 Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala  
 245 250 255  
 Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile  
 260 265 270  
 Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala  
 275 280 285  
 Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly  
 290 295 300  
 Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr  
 305 310 315 320  
 Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp  
 325 330 335  
 Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val  
 340 345 350  
 Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr  
 355 360 365

Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile  
 370 375 380  
 Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala  
 385 390 395 400  
 Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile  
 405 410 415  
 Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe  
 420 425 430  
 Asp Asn Tyr Ala Gly Glu Ala  
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 <223> RXA02562

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 Met Phe Leu Thr Lys  
 1 5  
 gtt tcg ctg ctt gat cat ccg gag tca ttg ccg ggg tat tta tcg agc 163  
 Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro Gly Tyr Leu Ser Ser  
 10 15 20  
 ctg gcg atc gtg gaa tat ctg cat gaa cag ccg ttg gag ttt cgt gca 211  
 Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro Leu Glu Phe Arg Ala  
 25 30 35  
 ccg att act gtg att act ggt gaa aat ggg gtg ggt aaa tcc acg ttg 259  
 Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys Ser Thr Leu  
 40 45 50  
 gtt gag gct ttg gcg gtg ggg atg cgc ctt aat ccg tct ggt ggc tct 307  
 Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn Pro Ser Gly Gly Ser  
 55 60 65  
 agg cat gca aac ttt ggc agg gaa ggc gat att gtg tcg tcg ctt cat 355  
 Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile Val Ser Ser Leu His  
 70 75 80 85  
 cag tcg ttg aag ttg gtg cgg aga gaa aac cct cgg gat gcg ttc ttt 403  
 Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro Arg Asp Ala Phe Phe  
 90 95 100  
 ttt cgg ggt gag acg atg tat aac gtg gct tcc tat tat gag gag tta 451  
 Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser Tyr Tyr Glu Glu Leu  
 105 110 115

atg ggg gaa aag aac atg cat gat ctt cac aag atg agc cat ggc gaa 499  
 Met Gly Glu Lys Asn Met His Asp Leu His Lys Met Ser His Gly Glu  
 120 125 130  
  
 tcg gta ttt gcg gtg att gat cgg cgt ttt aac aat caa gga ttt ttt 547  
 Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn Asn Gln Gly Phe Phe  
 135 140 145  
  
 gtt ttg gac gag cct gag gca ggc ctt tcc atg ctg agg cag ttg gag 595  
 Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met Leu Arg Gln Leu Glu  
 150 155 160 165  
  
 ttg ttg gga aag ttg ggc aac ctt gct cga ggt ggt gcg cag atc atc 643  
 Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly Gly Ala Gln Ile Ile  
 170 175 180  
  
 atg gct acg cac tct cca ata ttg ttg gct att ccg ggg gca gag atc 691  
 Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile Pro Gly Ala Glu Ile  
 185 190 195  
  
 ctt gaa att aca tct tcg ggt gtt gca aag gtg aat ttt gag gat gcg 739  
 Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val Asn Phe Glu Asp Ala  
 200 205 210  
  
 gag gct gtt cgt gcg gct cgg gaa ttt gtg gca gat ccg cga ggt acg 787  
 Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala Asp Pro Arg Gly Thr  
 215 220 225  
  
 gcg gcg ttt ctg act gcg gag gag gat cac caa tgatgcgta tatcacgat 840  
 Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln  
 230 235 240  
  
 att 843

<210> 82  
 <211> 240  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Gly Tyr Leu Ser Ser Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro  
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 Leu Glu Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val  
 35 40 45  
  
 Gly Lys Ser Thr Leu Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn  
 50 55 60  
  
 Pro Ser Gly Gly Ser Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile  
 65 70 75 80  
  
 Val Ser Ser Leu His Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro  
 85 90 95  
  
 Arg Asp Ala Phe Phe Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser  
 100 105 110

Tyr Tyr Glu Glu Leu Met Gly Glu Lys Asn Met His Asp Leu His Lys  
 115 120 125  
 Met Ser His Gly Glu Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn  
 130 135 140  
 Asn Gln Gly Phe Phe Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met  
 145 150 155 160  
 Leu Arg Gln Leu Glu Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly  
 165 170 175  
 Gly Ala Gln Ile Ile Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile  
 180 185 190  
 Pro Gly Ala Glu Ile Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val  
 195 200 205  
 Asn Phe Glu Asp Ala Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala  
 210 215 220  
 Asp Pro Arg Gly Thr Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln  
 225 230 235 240

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1006)  
 <223> RXA00950

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 Met Asn Thr Pro Ala  
 1 5  
 gtt cag gtt caa aat cta agt ttg agt ttt ggg tcg ttc aca gct gtc 163  
 Val Gln Val Gln Asn Leu Ser Leu Ser Phe Gly Ser Phe Thr Ala Val  
 10 15 20  
 aac ggc ctc agc ctc acg gtg gag cag ggg agc att cac ggc ttc ctc 211  
 Asn Gly Leu Ser Leu Thr Val Glu Gln Gly Ser Ile His Gly Phe Leu  
 25 30 35  
 ggc ccc aac ggt gca gga aag tca aca acc atc agg gca ctc att gga 259  
 Gly Pro Asn Gly Ala Gly Lys Ser Thr Thr Ile Arg Ala Leu Ile Gly  
 40 45 50  
 gtg cta aaa ccc caa aca ggt tca gtc gct att ctc ggc caa gat cct 307  
 Val Leu Lys Pro Gln Thr Gly Ser Val Ala Ile Leu Gly Gln Asp Pro  
 55 60 65  
 gtt gct cac ccc gat gtc ott cga aga gtt ggc tac gtt cca gga gat 355  
 Val Ala His Pro Asp Val Leu Arg Arg Val Gly Tyr Val Pro Gly Asp

70	75	80	85	
gcc aca ctg tgg gac aac ctc act ggg gcg gaa gtt ttc agg gcg ctc				403
Ala Thr Leu Trp Asp Asn Leu Thr Gly Ala Glu Val Phe Arg Ala Leu	90	95	100	
gaa tca ctc cgc aag act cca tcc aac cga gct cta gaa aac gag ctc				451
Glu Ser Leu Arg Lys Thr Pro Ser Asn Arg Ala Leu Glu Asn Glu Leu	105	110	115	
att gac gcc ttc caa ttg gat ccc tcg aag aag atc cgc gaa tac tcg				499
Ile Asp Ala Phe Gln Leu Asp Pro Ser Lys Lys Ile Arg Glu Tyr Ser	120	125	130	
aca ggt aac aga agg aaa gtc agt ctc atc gcg gcg ctc agt cat gag				547
Thr Gly Asn Arg Arg Lys Val Ser Leu Ile Ala Ala Leu Ser His Glu	135	140	145	
ccc gag ctc ctc atc gtt gac gag ccc acc gca ggc ttg gat ccc atc				595
Pro Glu Leu Leu Ile Val Asp Glu Pro Thr Ala Gly Leu Asp Pro Ile	150	155	160	165
atg gag caa gtc ttt gtc acc tat gtc cgc aag gca cga acc aac ggc				643
Met Glu Gln Val Phe Val Thr Tyr Val Arg Lys Ala Arg Thr Asn Gly	170	175	180	
gcg tcc gtg tta ctc agc agc cac att ctc agt gag gtg gag cag ctg				691
Ala Ser Val Leu Leu Ser Ser His Ile Leu Ser Glu Val Glu Gln Leu	185	190	195	
tgt gat tac gtc acg gtc ctt aaa gag ggg cga gca gtt gca tct aat				739
Cys Asp Tyr Val Thr Val Leu Lys Glu Gly Arg Ala Val Ala Ser Asn	200	205	210	
gag gtg agc tat ctg agg aag atc tcc gct cac cgc att act gcc acg				787
Glu Val Ser Tyr Leu Arg Lys Ile Ser Ala His Arg Ile Thr Ala Thr	215	220	225	
att ccg gcg gta cct caa cac ctt gct ggc agg gga gaa gtg gat ttc				835
Ile Pro Ala Val Pro Gln His Leu Ala Gly Arg Gly Glu Val Asp Phe	230	235	240	245
gat gct ggc cat ctc agc atc acc tgc gat gcc tcc gag gtt ccc gat				883
Asp Ala Gly His Leu Ser Ile Thr Cys Asp Ala Ser Glu Val Pro Asp	250	255	260	
att ttg cgc atc atc atc gac gct ggc ggc cag gac atc atc agc acc				931
Ile Leu Arg Ile Ile Ile Asp Ala Gly Gly Gln Asp Ile Ile Ser Thr	265	270	275	
gcg gcg tcg ctg gag gag atc ttc ttg cgt cac tat gga gaa acc gtg				979
Ala Ala Ser Leu Glu Glu Ile Phe Leu Arg His Tyr Gly Glu Thr Val	280	285	290	
agt ggt tca gaa agc aag gca tca caa tgatccgtct taatctacgt ctt				1029
Ser Gly Ser Glu Ser Lys Ala Ser Gln	295	300		

<210> 84  
 <211> 302

<213> Corynebacterium glutamicum

Met 1	Asn	Thr	Pro	Ala 5	Val	Gln	Val	Gln	Asn 10	Leu	Ser	Leu	Ser	Phe 15	Gly
Ser	Phe	Thr	Ala 20	Val	Asn	Gly	Leu	Ser 25	Leu	Thr	Val	Glu	Gln 30	Gly	Ser
Ile	His 35	Gly	Phe	Leu	Gly	Pro	Asn 40	Gly	Ala	Gly	Lys 45	Ser	Thr	Thr	Ile
Arg	Ala 50	Leu	Ile	Gly	Val	Leu 55	Lys	Pro	Gln	Thr	Gly 60	Ser	Val	Ala	Ile
Leu 65	Gly	Gln	Asp	Pro	Val 70	Ala	His	Pro	Asp	Val 75	Leu	Arg	Arg	Val	Gly 80
Tyr	Val	Pro	Gly 85	Asp	Ala	Thr	Leu	Trp 90	Asp	Asn	Leu	Thr	Gly	Ala 95	Glu
Val	Phe	Arg	Ala 100	Leu	Glu	Ser	Leu	Arg 105	Lys	Thr	Pro	Ser	Asn 110	Arg	Ala
Leu	Glu 115	Asn	Glu	Leu	Ile	Asp	Ala 120	Phe	Gln	Leu	Asp	Pro 125	Ser	Lys	Lys
Ile 130	Arg	Glu	Tyr	Ser	Thr	Gly 135	Asn	Arg	Arg	Lys	Val 140	Ser	Leu	Ile	Ala
Ala 145	Leu	Ser	His	Glu	Pro 150	Glu	Leu	Leu	Ile	Val 155	Asp	Glu	Pro	Thr	Ala 160
Gly	Leu	Asp	Pro 165	Ile	Met	Glu	Gln	Val 170	Phe	Val	Thr	Tyr	Val 175	Arg	Lys
Ala	Arg	Thr	Asn 180	Gly	Ala	Ser	Val	Leu 185	Leu	Ser	Ser	His	Ile 190	Leu	Ser
Glu	Val 195	Glu	Gln	Leu	Cys	Asp	Tyr 200	Val	Thr	Val	Leu	Lys 205	Glu	Gly	Arg
Ala 210	Val	Ala	Ser	Asn	Glu 215	Val	Ser	Tyr	Leu	Arg	Lys 220	Ile	Ser	Ala	His
Arg 225	Ile	Thr	Ala	Thr	Ile 230	Pro	Ala	Val	Pro	Gln 235	His	Leu	Ala	Gly	Arg 240
Gly	Glu	Val	Asp 245	Phe	Asp	Ala	Gly	His 250	Leu	Ser	Ile	Thr	Cys 255	Asp	Ala
Ser	Glu	Val	Pro 260	Asp	Ile	Leu	Arg	Ile 265	Ile	Ile	Asp	Ala	Gly 270	Gly	Gln
Asp	Ile 275	Ile	Ser	Thr	Ala	Ala	Ser 280	Leu	Glu	Glu	Ile	Phe 285	Leu	Arg	His
Tyr	Gly 290	Glu	Thr	Val	Ser	Gly 295	Ser	Glu	Ser	Lys 300	Ala	Ser	Gln		

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att 643  
Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile  
170 175 180



gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag	691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu	
185 190 195	
caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc	739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val	
200 205 210	
agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa	787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu	
215 220 225	
ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat	835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp	
230 235 240 245	
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa	883
Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln	
250 255 260	
tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga	931
Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg	
265 270 275	
acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt	979
Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg	
280 285 290	
gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt	1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser	
295 300 305	
gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg	1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg	
310 315 320 325	
tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc	1123
Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser	
330 335 340	
gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat	1171
Val Gly Lys Ala Ser Arg Ser Ser Val Val Ser Thr Leu Asn Asp	
345 350 355	
gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa	1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln	
360 365 370	
gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt	1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly	
375 380 385	
aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc	1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser	
390 395 400 405	
ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag	1363
Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln	
410 415 420	

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411  
 Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu  
                   425                                  430                                  435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg 1459  
 Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala  
                   440                                  445                                  450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta 1507  
 Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu  
                   455                                  460                                  465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg 1555  
 Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg  
                   470                                  475                                  480                                  485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603  
 Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu  
                                   490                                  495                                  500

gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg 1651  
 Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val  
                                   505                                  510                                  515

ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc 1699  
 Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr  
                                   520                                  525                                  530

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta 1741  
 Asn Arg Arg Trp His Val Glu Ala Gly Glu Val Arg Glu Leu  
                   535                                  540                                  545

taaccgtttc cgtattgatg cca 1764

<210> 86  
 <211> 547  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 86  
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Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val  
                   20                                  25                                  30

Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys  
                   35                                  40                                  45

Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser  
                   50                                  55                                  60

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr  
                   65                                  70                                  75                                  80

Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln  
                                   85                                  90                                  95

Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp  
                   100                                  105                                  110

Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg  
 115 120 125  
 Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val  
 130 135 140  
 Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly  
 145 150 155 160  
 Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu  
 165 170 175  
 Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp  
 180 185 190  
 Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly  
 195 200 205  
 Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val  
 210 215 220  
 Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr  
 225 230 235 240  
 Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln  
 245 250 255  
 His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu  
 260 265 270  
 Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg  
 275 280 285  
 Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala  
 290 295 300  
 Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu  
 305 310 315 320  
 Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp  
 325 330 335  
 Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val  
 340 345 350  
 Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly  
 355 360 365  
 Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly  
 370 375 380  
 Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn  
 385 390 395 400  
 Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile  
 405 410 415  
 Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu  
 420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val  
 435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg  
 450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala  
 465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr  
 485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala  
 500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu  
 515 520 525

Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val  
 530 535 540

Arg Glu Leu  
 545

<210> 87  
 <211> 981  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> RXA01185

<400> 87  
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catagccgcc gacacgtgaa tcgaaagaag ttcattctccg atg act gat cct gaa 115  
 Met Thr Asp Pro Glu  
 1 5

aac tcg caa gga acc cca cag att tgt ccg act gat ccg act acg caa 163  
 Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr Asp Pro Thr Thr Gln  
 10 15 20

gca tta gca gtt cgg ggc tta acc aag tcc tat ggt gat gca aca gta 211  
 Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr Gly Asp Ala Thr Val  
 25 30 35

gtg aac aat atc aat ctg gac atc ccc aaa gga gcc att tac ggc atc 259  
 Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly Ala Ile Tyr Gly Ile  
 40 45 50

gtt gga cct aat ggt gca ggt aaa acc acc atg ctg tcc atg gca acg 307  
 Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met Leu Ser Met Ala Thr  
 55 60 65

ggt tta ctg agg ccg aat aaa ggc acc gcg tgg att tcg ggt ttc aat 355  
 Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp Ile Ser Gly Phe Asn  
 70 75 80 85

gtg tgg gaa gag cca aac gat gca aaa cga agc atg gga ttg ttg gca 403  
 Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser Met Gly Leu Leu Ala  
                     90                    95                    100

gat ggc ttg ccc atc ttt gat cgc ttg act ggc aaa gaa ctg ctc aca 451  
 Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly Lys Glu Leu Leu Thr  
                     105                    110                    115

tat gtc ggg gca ttg cgt gag ttg gat gaa ggc att gtt gat caa cgt 499  
 Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly Ile Val Asp Gln Arg  
                     120                    125                    130

agt gag gaa ttg ctg gag gcc ctc ggg ctt aaa gaa gca gcg ggc aag 547  
 Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys Glu Ala Ala Gly Lys  
                     135                    140                    145

aga gtc gtc gac tat tcc gcc ggc atg acg aag aag att ctt ttg gcc 595  
 Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys Lys Ile Leu Leu Ala  
                     150                    155                    160                    165

cag gcc ctc att cac aat ccg aaa gtg ctc atc ctt gat gaa cct ttg 643  
 Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile Leu Asp Glu Pro Leu  
                     170                    175                    180

gaa gcg gtt gat ccg gtg tct ggt cgt ttg att cag cag att ttg aag 691  
 Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile Gln Gln Ile Leu Lys  
                     185                    190                    195

aac ttt gcg caa acg ggt gga acc gtc gtt ttg agt tcg cat gtc atg 739  
 Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu Ser Ser His Val Met  
                     200                    205                    210

gaa ttg gtt gag ggg ttg tgc gat cac gtt gcc atc atc aac agg gga 787  
 Glu Leu Val Glu Gly Leu Cys Asp His Val Ala Ile Ile Asn Arg Gly  
                     215                    220                    225

gtg gtg gag att gcc gga cat gtg aat gag gtt cgt cgg ggc aga tct 835  
 Val Val Glu Ile Ala Gly His Val Asn Glu Val Arg Arg Gly Arg Ser  
                     230                    235                    240                    245

tac cgg atg tct tcg tta atg cgg ttg aag gcg ctg ctc ttc aag agg 883  
 Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala Leu Leu Phe Lys Arg  
                     250                    255                    260

ggt cac tat ctt ggt tgg gtg cgt ccg aag gcc ata gcg aag gcc aaa 931  
 Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala Ile Ala Lys Ala Lys  
                     265                    270                    275

atc aga acg agg atc ggg ctg agt aaa tgactaaaac acttctgaaa cta 981  
 Ile Arg Thr Arg Ile Gly Leu Ser Lys  
                     280                    285

<210> 88

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met Thr Asp Pro Glu Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr

1	5	10	15
Asp Pro Thr Thr Gln Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr	20	25	30
Gly Asp Ala Thr Val Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly	35	40	45
Ala Ile Tyr Gly Ile Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met	50	55	60
Leu Ser Met Ala Thr Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp	65	70	75
Ile Ser Gly Phe Asn Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser	85	90	95
Met Gly Leu Leu Ala Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly	100	105	110
Lys Glu Leu Leu Thr Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly	115	120	125
Ile Val Asp Gln Arg Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys	130	135	140
Glu Ala Ala Gly Lys Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys	145	150	155
Lys Ile Leu Leu Ala Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile	165	170	175
Leu Asp Glu Pro Leu Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile	180	185	190
Gln Gln Ile Leu Lys Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu	195	200	205
Ser Ser His Val Met Glu Leu Val Glu Gly Leu Cys Asp His Val Ala	210	215	220
Ile Ile Asn Arg Gly Val Val Glu Ile Ala Gly His Val Asn Glu Val	225	230	235
Arg Arg Gly Arg Ser Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala	245	250	255
Leu Leu Phe Lys Arg Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala	260	265	270
Ile Ala Lys Ala Lys Ile Arg Thr Arg Ile Gly Leu Ser Lys	275	280	285

&lt;210&gt; 89

&lt;211&gt; 1203

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1180)

&lt;223&gt; RXN00412

&lt;400&gt; 89

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cttttgacga acaccacgtc gcgtacgctt cctcggggag ttaaactatt tgtcttccag 60

cttttgcccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
                               Val Ser His Thr Ala
                               1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
                               10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
                               25 30 35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
                               40 45 50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc 307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
                               55 60 65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg 355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
                               70 75 80 85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
                               90 95 100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
                               105 110 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
                               120 125 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc 547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
                               135 140 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg 595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
                               150 155 160 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc 643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
                               170 175 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca 691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
                               185 190 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa 739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
                               200 205 210

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ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt 787  
 Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg  
 215 220 225  
  
 tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa 835  
 Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu  
 230 235 240 245  
  
 tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct 883  
 Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala  
 250 255 260  
  
 caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931  
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu  
 265 270 275  
  
 tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979  
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu  
 280 285 290  
  
 act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027  
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln  
 295 300 305  
  
 ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075  
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg  
 310 315 320 325  
  
 caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123  
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala  
 330 335 340  
  
 att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171  
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu  
 345 350 355  
  
 atc acc cga tgaacgagat gatcctcgca gct 1203  
 Ile Thr Arg  
 360

&lt;210&gt; 90

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 90

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln  
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys  
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser  
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser



65	70	75	80
Pro Thr Ser Gly	Ser Leu Leu Leu Asn Gly	Thr Asp Ile Val Gly	Met
	85	90	95
Pro Glu Ser Lys	Leu Arg Lys Leu Arg Ser Asn Ile Gly	Met Ile Phe	
	100	105	110
Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu			
	115	120	125
Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg			
	130	135	140
Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn			
	145	150	155
Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala			
	165	170	175
Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr			
	180	185	190
Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg			
	195	200	205
Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu			
	210	215	220
Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser			
	225	230	235
Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro			
	245	250	255
Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr			
	260	265	270
Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu			
	275	280	285
Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala			
	290	295	300
Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val			
	305	310	315
Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr			
	325	330	335
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr			
	340	345	350
Thr Thr Ile Lys Glu Ile Thr Arg			
	355	360	

&lt;210&gt; 91

&lt;211&gt; 1203

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1180)

&lt;223&gt; FRXA00412

&lt;400&gt; 91

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cttttgacga acaccacgtc gcgtacgctt cctcggggcg ttaaactatt tgtcttccag 60

cttttgcccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
                                   Val Ser His Thr Ala
                                   1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
                                   10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
                                   25 30 35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
                                   40 45 50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc 307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
                                   55 60 65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg 355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
                                   70 75 80 85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
                                   90 95 100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
                                   105 110 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
                                   120 125 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc 547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
                                   135 140 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg 595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
                                   150 155 160 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc 643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
                                   170 175 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca 691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
                                   185 190 195

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gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa 739  
 Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu  
 200 205 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt 787  
 Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg  
 215 220 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa 835  
 Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu  
 230 235 240 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct 883  
 Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala  
 250 255 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931  
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu  
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979  
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu  
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027  
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln  
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075  
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg  
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123  
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala  
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171  
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu  
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203  
 Ile Thr Arg  
 360

&lt;210&gt; 92

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 92

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln  
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys  
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser

50	55	60
Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser 65 70 75 80		
Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met 85 90 95		
Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe 100 105 110		
Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu 115 120 125		
Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg 130 135 140		
Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn 145 150 155 160		
Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala 165 170 175		
Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr 180 185 190		
Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg 195 200 205		
Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu 210 215 220		
Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser 225 230 235 240		
Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro 245 250 255		
Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr 260 265 270		
Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu 275 280 285		
Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala 290 295 300		
Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val 305 310 315 320		
Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr 325 330 335		
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr 340 345 350		
Thr Thr Ile Lys Glu Ile Thr Arg 355 360		

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<220>
<221> CDS
<222> (101)..(2317)
<223> RXN02925
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<400> 93																
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catcatctcg accccgaccg ggttgagcgg aaggaacctc atg agc act ccc cac 115																
Met Ser Thr Pro His 5																
cac cac ggt gat cac ccc gct ccg gaa aca gac cac acc cac cac ccg 163																
His His Gly Asp His Pro Ala Pro Glu Thr Asp His Thr His His Pro 20																
aat cat gcc ggt cac gag cac cat gcg gat gcc gcc acc cac ggc cag 211																
Asn His Ala Gly His Glu His His Ala Asp Ala Ala Thr His Gly Gln 35																
gcc atg ccg cac gat cat ccg cat tcc act gtc gat gaa gaa cat cag 259																
Ala Met Pro His Asp His Pro His Ser Thr Val Asp Glu Glu His Gln 50																
gtc cac agt cac ggt gaa cac gcc ggc cac agc gcc gcg atg ttc ccg 307																
Val His Ser His Gly Glu His Ala Gly His Ser Ala Ala Met Phe Arg 65																
gac cgc ttc tgg tgg tcg ctg atc ctg tcg gtt ccg gtg gtg ttc ttc 355																
Asp Arg Phe Trp Trp Ser Leu Ile Leu Ser Val Pro Val Val Phe Phe 85																
agc ccg atg ttc gcc gac ctg ctg gga tat aat att ccg gag att ccg 403																
Ser Pro Met Phe Ala Asp Leu Leu Gly Tyr Asn Ile Pro Glu Ile Pro 100																
gga gcc tac tgg att cct ccg gtc ctg ggc acg atc atc ttc ctc tac 451																
Gly Ala Tyr Trp Ile Pro Pro Val Leu Gly Thr Ile Ile Phe Leu Tyr 115																
ggc ggc acc ccc ttc ctc aag ggc gca atg acc gag ctg aaa tcc cgc 499																
Gly Gly Thr Pro Phe Leu Lys Gly Ala Met Thr Glu Leu Lys Ser Arg 130																
caa ccg ggc atg atg ctc ctg atc gcc atg gcg atc acc gtg gcg ttt 547																
Gln Pro Gly Met Met Leu Leu Ile Ala Met Ala Ile Thr Val Ala Phe 145																
atc gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggc ttc cac cta gat 595																
Ile Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp 165																
ttc tgg tgg gaa ctg gcc ctg ctg gtg acc atc atg ctg ttg ggc cac 643																
Phe Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His 180																
tgg ctg gag atg cgc gct ctt ggt qca gcc tcc tcc gcg ctt gac gcg 691																

Trp	Leu	Glu	Met	Arg	Ala	Leu	Gly	Ala	Ala	Ser	Ser	Ala	Leu	Asp	Ala		
			185					190					195				
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Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met  
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Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu

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Thr	Lys	Ala	Lys	Gly	Gln	Ser	Ser	Glu	Ala	Leu	Arg	Lys	Leu	Leu	Asp
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Thr	Thr	Gly	Thr	Met	Ser	Val	Thr	Asp	Val	Thr	Ala	Ile	Asn	Tyr	Ser
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Glu	Thr	Glu	Ile	Leu	Glu	Phe	Ala	Ala	Ala	Val	Glu	Ser	Ala	Ser	Glu
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His	Pro	Ile	Ala	Gln	Ala	Ile	Ala	Lys	Ala	Ala	Glu	His	Glu	Gln	Val
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Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu						
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Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala						
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Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg						
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Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro						
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Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro Gly Glu Lys Ile Ala	280	285	290	
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Val Glu Arg Lys Leu Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn  
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Tyr Ala Thr Glu Ser Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser  
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Pro Glu Gln Leu Ile Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe  
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Asp Leu Lys His Arg Val Ile Val Ser Ala Leu Leu Ser Val Pro Val  
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Val Leu Val Ser Met Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp  
                     130                    135                    140

Ala Val Leu Thr Leu Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro  
                     145                    150                    155                    160

Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met  
                     165                    170                    175

Asn Thr Leu Val Ser Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu  
                     180                    185                    190

Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu  
                     195                    200                    205

Met His Leu Leu Pro Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu  
                     210                    215                    220

Thr Val Ala Val Val Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu  
                     225                    230                    235                    240



Thr Lys Ala Lys Gly Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp  
 245 250 255  
 Met Gly Ala Lys Asp Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg  
 260 265 270  
 Val Pro Val Asn Gln Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro  
 275 280 285  
 Gly Glu Lys Ile Ala Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala  
 290 295 300  
 Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr  
 305 310 315 320  
 Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu  
 325 330 335  
 Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met  
 340 345 350  
 Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg  
 355 360 365  
 Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile  
 370 375 380  
 Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu  
 385 390 395 400  
 Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro  
 405 410 415  
 Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly  
 420 425 430  
 Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu  
 435 440 445  
 Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val  
 450 455 460  
 Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser  
 465 470 475 480  
 Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu  
 485 490 495  
 His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val  
 500 505 510  
 Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg  
 515 520 525  
 Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala  
 530 535 540  
 Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val  
 545 550 555 560

Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp  
565 570 575

Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu  
580 585 590

Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys  
595 600 605

Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu  
610 615 620

Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys  
625 630 635 640

Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala  
645 650 655

Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile  
660 665 670

Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val  
675 680 685

Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn  
690 695 700

Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala  
705 710 715 720

Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser  
725 730 735

Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala  
740 745 750

Arg Ser Asn  
755

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<211> 1830  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1807)  
<223> RXN00702

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gtcgaaaagc aataaatagc ccagaaaggg ccgaagttaa atg agt gct cct ttt 115  
Met Ser Ala Pro Phe  
1 5

agc gcg cgc act gcg tgg tcg acg gac ccc gtg ctg gaa ctg gaa agc 163  
Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val Leu Glu Leu Glu Ser  
10 15 20

gtc gct gcc tcg tat tat gac gat gag cgc acg ctg gcg gcg ccg cag	211
Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr Leu Ala Ala Pro Gln	
25 30 35	
atc agc gac gtg aat ctg acg ctt ttt gaa ggc gaa atc ctg ctg gtt	259
Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly Glu Ile Leu Leu Val	
40 45 50	
gtg ggg cgc acc ggc tcc ggc aaa tcg acg ctg ctg aac gcg atg tcc	307
Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu Leu Asn Ala Met Ser	
55 60 65	
ggc gcg atg ccg cat gcg acc ggc ggc cga ctt gat ggg cgc gtg cgc	355
Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu Asp Gly Arg Val Arg	
70 75 80 85	
gtg gtc ggc cgg gat acg cgt gat ttc cca cca cgc atg ctt tcc gac	403
Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro Arg Met Leu Ser Asp	
90 95 100	
gtg gtc ggc gtc gtt ggg caa gat ccg gcg gca agt ttt atc acc aac	451
Val Val Gly Val Val Gly Gln Asp Pro Ala Ala Ser Phe Ile Thr Asn	
105 110 115	
acg gtt gaa gaa gaa ctt gcc tac agc atg gag caa tta ggg ctc cca	499
Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu Gln Leu Gly Leu Pro	
120 125 130	
cct gcg gtc atg cgc aag cgc gta gag gaa acc ctt gat ctt tta ggc	547
Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu Asp Leu Leu Gly	
135 140 145	
atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta tct ggt ggt gag	595
Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu Ser Gly Gly Glu	
150 155 160 165	
cag cag cgc gtg gcg att ggc gcg gtg ctg acc act cgc ccc gcg ctg	643
Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr Arg Pro Ala Leu	
170 175 180	
att atc ttg gat gaa cca acc agc gct ttg gac cct aat ggt gcc gag	691
Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Asn Gly Ala Glu	
185 190 195	
gat gtg ctg gca acc gta acc aag ctg gct cat gac ttg gcg atg acc	739
Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp Leu Ala Met Thr	
200 205 210	
gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg cag tac gtg gac	787
Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu Gln Tyr Val Asp	
215 220 225	
cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act gtt ggg acg ccg	835
Arg Val Ala His Val Gly Ala Asp Gly His Val Thr Val Gly Thr Pro	
230 235 240 245	
gaa gaa atc atg gct gat tct gat gtg gca cca ccc att gtg gaa tta	883
Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro Ile Val Glu Leu	
250 255 260	
gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg atc cgc gat gca	931

Gly	Arg	Trp	Ala	Gly	Trp	Ala	Pro	Leu	Pro	Leu	Ser	Ile	Arg	Asp	Ala		
			265					270					275				
cgc	gca	cac	tcc	gct	gac	atg	cgc	aaa	cgc	ctg	tat	cag	cgt	ggt	tta	979	
Arg	Ala	His	Ser	Ala	Asp	Met	Arg	Lys	Arg	Leu	Tyr	Gln	Arg	Gly	Leu		
		280					285					290					
gtg	gtg	aac	aaa	tta	cac	aac	cac	gct	gtc	cag	cca	ctt	ttg	atc	gcc	1027	
Val	Val	Asn	Lys	Leu	His	Asn	His	Ala	Val	Gln	Pro	Leu	Leu	Ile	Ala		
		295				300					305						
gaa	gat	atc	atg	gtt	gat	ttc	ccc	gaa	atc	cgt	gcc	gtt	gac	ggc	gtg	1075	
Glu	Asp	Ile	Met	Val	Asp	Phe	Pro	Glu	Ile	Arg	Ala	Val	Asp	Gly	Val		
310					315					320					325		
aac	ttg	aat	ctc	aac	tcc	ggt	gaa	att	acc	gtg	ctc	atg	ggc	cga	aac	1123	
Asn	Leu	Asn	Leu	Asn	Ser	Gly	Glu	Ile	Thr	Val	Leu	Met	Gly	Arg	Asn		
				330					335					340			
ggc	tgc	gga	aaa	tca	tcc	ctg	ctg	tgg	gct	tta	caa	ggt	tca	ggg	act	1171	
Gly	Cys	Gly	Lys	Ser	Ser	Leu	Leu	Trp	Ala	Leu	Gln	Gly	Ser	Gly	Thr		
			345					350					355				
aga	aat	cag	ggc	tgc	gtg	cag	gtg	ctt	gat	gag	gcc	gcg	gga	ttt	tgc	1219	
Arg	Asn	Gln	Gly	Ser	Val	Gln	Val	Leu	Asp	Glu	Ala	Ala	Gly	Phe	Ser		
		360					365					370					
tgg	aca	gac	ccc	aaa	act	tta	aag	ccc	gcc	aag	cgg	cgc	aat	ctt	gtg	1267	
Trp	Thr	Asp	Pro	Lys	Thr	Leu	Lys	Pro	Ala	Lys	Arg	Arg	Asn	Leu	Val		
		375				380					385						
tcc	atg	gtt	cgc	caa	aca	ccg	acc	gat	att	ttg	tat	gaa	tca	acc	gtg	1315	
Ser	Met	Val	Pro	Gln	Thr	Pro	Thr	Asp	Ile	Leu	Tyr	Glu	Ser	Thr	Val		
390					395					400					405		
cat	gca	gag	ctc	gca	cgc	tct	gat	aaa	gat	gcc	gca	gca	ccc	gcc	ggc	1363	
His	Ala	Glu	Leu	Ala	Arg	Ser	Asp	Lys	Asp	Ala	Ala	Ala	Pro	Ala	Gly		
				410					415					420			
acc	acg	cgg	gaa	atc	ctg	gat	tca	ctg	gtc	ccg	aat	atc	ccg	gac	cat	1411	
Thr	Thr	Arg	Glu	Ile	Leu	Asp	Ser	Leu	Val	Pro	Asn	Ile	Pro	Asp	His		
			425					430					435				
ctc	cac	cca	cgt	gat	cta	tca	gaa	ggc	caa	aag	ctc	tcc	ctc	gcg	ctg	1459	
Leu	His	Pro	Arg	Asp	Leu	Ser	Glu	Gly	Gln	Lys	Leu	Ser	Leu	Ala	Leu		
		440					445					450					
tcc	atc	caa	ctc	gcc	gca	aaa	ccc	cgc	gtg	gta	ttt	ttc	gac	gaa	ccc	1507	
Ser	Ile	Gln	Leu	Ala	Ala	Lys	Pro	Arg	Val	Val	Phe	Phe	Asp	Glu	Pro		
		455				460					465						
acc	cgc	ggc	cta	gac	tac	gac	ggc	aag	aaa	tcc	ctc	gcc	cgc	tcc	ttc	1555	
Thr	Arg	Gly	Leu	Asp	Tyr	Asp	Gly	Lys	Lys	Ser	Leu	Ala	Arg	Ser	Phe		
470					475					480					485		
caa	caa	ctc	gca	gac	gac	ggc	cac	gcc	att	ttg	gtg	gtc	acc	cac	gac	1603	
Gln	Gln	Leu	Ala	Asp	Asp	Gly	His	Ala	Ile	Leu	Val	Val	Thr	His	Asp		
			490						495						500		
gtg	gaa	ttc	tct	gca	ctg	tgc	gcc	gac	cga	gtg	ttg	ttt	atg	gcc	tct	1651	
Val	Glu	Phe	Ser	Ala	Leu	Cys	Ala	Asp	Arg	Val	Leu	Phe	Met	Ala	Ser		

505	510	515	
gga aag atc atc tcc gat ggc aca gcc gta gaa atc ctc ccc gca tca			1699
Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile Leu Pro Ala Ser			
520	525	530	
ccg gct tac gcc cca caa gtc gca aaa atc acc gcc ggc atc caa gag			1747
Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala Gly Ile Gln Glu			
535	540	545	
gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct gcg cta ggg cat			1795
Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala Ala Leu Gly His			
550	555	560	565
ggt gaa atc tca tgatcaacgc catcacactc aag			1830
Gly Glu Ile Ser			

&lt;210&gt; 104

&lt;211&gt; 569

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 104

Met Ser Ala Pro Phe Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val			
1	5	10	15
Leu Glu Leu Glu Ser Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr			
20	25	30	
Leu Ala Ala Pro Gln Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly			
35	40	45	
Glu Ile Leu Leu Val Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu			
50	55	60	
Leu Asn Ala Met Ser Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu			
65	70	75	80
Asp Gly Arg Val Arg Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro			
85	90	95	
Arg Met Leu Ser Asp Val Val Gly Val Val Gly Gln Asp Pro Ala Ala			
100	105	110	
Ser Phe Ile Thr Asn Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu			
115	120	125	
Gln Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr			
130	135	140	
Leu Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu			
145	150	155	160
Leu Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr			
165	170	175	
Thr Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp			
180	185	190	

Pro Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His  
 195 200 205  
 Asp Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val  
 210 215 220  
 Leu Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val  
 225 230 235 240  
 Thr Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro  
 245 250 255  
 Pro Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu  
 260 265 270  
 Ser Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu  
 275 280 285  
 Tyr Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln  
 290 295 300  
 Pro Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg  
 305 310 315 320  
 Ala Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val  
 325 330 335  
 Leu Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu  
 340 345 350  
 Gln Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu  
 355 360 365  
 Ala Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys  
 370 375 380  
 Arg Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu  
 385 390 395 400  
 Tyr Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala  
 405 410 415  
 Ala Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro  
 420 425 430  
 Asn Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys  
 435 440 445  
 Leu Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val  
 450 455 460  
 Phe Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser  
 465 470 475 480  
 Leu Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu  
 485 490 495  
 Val Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val  
 500 505 510  
 Leu Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu

515                      520                      525  
 Ile Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr  
 530                      535                      540  
 Ala Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys  
 545                      550                      555                      560  
 Ala Ala Leu Gly His Gly Glu Ile Ser  
 565  
  
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 <213> Corynebacterium glutamicum  
  
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 <223> FRXA00702  
  
 <400> 105  
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 Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu  
 1                      5                      10                      15  
 gat ctt tta ggc atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta 96  
 Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu  
 20                      25                      30  
 tct ggt ggt gag cag cag cgc gtg gcg att ggc gcg gtg ctg acc act 144  
 Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr  
 35                      40                      45  
 cgc ccc gcg ctg att atc ttg gat gaa cca acc agc gct ttg gac cct 192  
 Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro  
 50                      55                      60  
 aat ggt gcc gag gat gtg ctg gca acc gta acc aag ctg gct cat gac 240  
 Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp  
 65                      70                      75                      80  
 ttg gcg atg acc gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg 288  
 Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu  
 85                      90                      95  
 cag tac gtg gac cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act 336  
 Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr  
 100                      105                      110  
 gtt ggg acg ccg gaa gaa atc atg gct gat tct gat gtg gca cca ccc 384  
 Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro  
 115                      120                      125  
 att gtg gaa tta gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg 432  
 Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser  
 130                      135                      140  
 atc cgc gat gca cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat 480  
 Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr

145	150	155	160	
cag cgt ggt tta gtg gtg aac aaa tta cac aac cac gct gtc cag cca				528
Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro				
	165	170	175	
ctt ttg atc gcc gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc				576
Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala				
	180	185	190	
gtt gac ggc gtg aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc				624
Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu				
	195	200	205	
atg ggc cga aac ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa				672
Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln				
	210	215	220	
ggt tca ggg act aga aat cag ggc tgc gtg cag gtg ctt gat gag gcc				720
Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala				
	225	230	235	240
gcg gga ttt tcg tgg aca gac ccc aaa act tta aag ccc gcc aag cgg				768
Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg				
	245	250	255	
cgc aat ctt gtg tcc atg gtt ccg caa aca ccg acc gat att ttg tat				816
Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr				
	260	265	270	
gaa tca acc gtg cat gca gag ctc gca cgc tct gat aaa gat gcc gca				864
Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala				
	275	280	285	
gca ccc gcc ggc acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat				912
Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn				
	290	295	300	
atc ccg gac cat ctc cac cca cgt gat cta tca gaa ggc caa aag ctc				960
Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu				
	305	310	315	320
tcc ctc gcg ctg tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt				1008
Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe				
	325	330	335	
ttc gac gaa ccc acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc				1056
Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu				
	340	345	350	
gcc cgc tcc ttc caa caa ctc gca gac gac ggc cac gcc att ttg gtg				1104
Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val				
	355	360	365	
gtc acc cac gac gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg				1152
Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu				
	370	375	380	
ttt atg gcc tct gga aag atc atc tcc gat ggc aca gcc gta gaa atc				1200
Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile				
	385	390	395	400



ctc ccc gca tca ccg gct tac gcc cca caa gtc gca aaa atc acc gcc 1248  
 Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala  
                   405                                  410                                  415

ggc atc caa gag gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct 1296  
 Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala  
                   420                                  425                                  430

gcg cta ggg cat ggt gaa atc tca tgatcaacgc catcacactc aag 1343  
 Ala Leu Gly His Gly Glu Ile Ser  
                   435                                  440

<210> 106

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu  
   1                                  5                                  10                                  15

Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu  
                   20                                  25                                  30

Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr  
                   35                                  40                                  45

Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro  
                   50                                  55                                  60

Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp  
   65                                  70                                  75                                  80

Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu  
                   85                                  90                                  95

Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr  
                   100                                  105                                  110

Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro  
                   115                                  120                                  125

Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser  
                   130                                  135                                  140

Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr  
   145                                  150                                  155                                  160

Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro  
                   165                                  170                                  175

Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala  
                   180                                  185                                  190

Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu  
                   195                                  200                                  205

Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln  
                   210                                  215                                  220

Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala  
 225 230 235 240  
 Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg  
 245 250 255  
 Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr  
 260 265 270  
 Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala  
 275 280 285  
 Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn  
 290 295 300  
 Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu  
 305 310 315 320  
 Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe  
 325 330 335  
 Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu  
 340 345 350  
 Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val  
 355 360 365  
 Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu  
 370 375 380  
 Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile  
 385 390 395 400  
 Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala  
 405 410 415  
 Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala  
 420 425 430  
 Ala Leu Gly His Gly Glu Ile Ser  
 435 440

<210> 107  
 <211> 576  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(553)  
 <223> RXN00828

<400> 107  
 cggatgatcac cgggcccgaat ggcgctggaa aatccacact tgcgctgacc atgggtggat 60  
 tgcttccgcg aaaagtgggc agctggaact ctctgacacg gtg cgc ggc ggc ctt 115  
 Val Arg Gly Gly Leu  
 1 5

aac acg ccc ccg cac aag tgg cgt tca gct gat cta gct gca cgt att 163  
 Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp Leu Ala Ala Arg Ile  
                     10                    15                    20

ggc act gtc ttt cag gat cca gag cac caa ttt gtg gcg cgc act gtg 211  
 Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe Val Ala Arg Thr Val  
                     25                    30                    35

cgt gat gag cta gaa att ggg ccg aaa atc atg aaa gtc gat gca agc 259  
 Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met Lys Val Asp Ala Ser  
                     40                    45                    50

gag cgc atc gag gag ctg ctt gat cgt ttg cgc ctc cgc cac ttg gaa 307  
 Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg Leu Arg His Leu Glu  
                     55                    60                    65

aac gcc aat ccg ttt acc ttg agt ggt gga gaa aag cgc cgc cta tct 355  
 Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu Lys Arg Arg Leu Ser  
                     70                    75                    80                    85

gtg gcg aca gcc ttg gtg gca gca ccg aaa ctt ctc att ttg gat gag 403  
 Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu Leu Ile Leu Asp Glu  
                     90                    95                    100

cct acg ttt ggc caa gat ccc gag acc ttc aca gag ctg gtg acg atg 451  
 Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr Glu Leu Val Thr Met  
                     105                    110                    115

ttg cgt gaa tta aca gac aac gga atc agc att gtg tcg gta acc cat 499  
 Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile Val Ser Val Thr His  
                     120                    125                    130

gat cct gat ttc atc gca gcg ctg ggc gat cac cac att gag gtg agc 547  
 Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His His Ile Glu Val Ser  
                     135                    140                    145

gcg aag tgaacctgct gatcaaaatt aat 576  
 Ala Lys  
 150

&lt;210&gt; 108

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 108

Val Arg Gly Gly Leu Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp  
                     1                    5                    10                    15

Leu Ala Ala Arg Ile Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe  
                     20                    25                    30

Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met  
                     35                    40                    45

Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg  
                     50                    55                    60

Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu  
                     65                    70                    75                    80

Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu  
85 90 95

Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr  
100 105 110

Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile  
115 120 125

Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His  
130 135 140

His Ile Glu Val Ser Ala Lys  
145 150

<210> 109

<211> 392

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(369)

<223> FRXA00828

<400> 109

gag cac caa ttt gtg gcg cgc act gtg cgt gat gag cta gaa att ggt 48  
Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly  
1 5 10 15

ccg aaa atc atg aaa gtt gat gca agc gag cgc atc gag gag ttg ctt 96  
Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu  
20 25 30

gat cgg ttg cgc ctc cgc cac tta gaa aat gct aat ccg ttt acc ttg 144  
Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu  
35 40 45

agt ggt gga gaa aag cgc cgc cta tct gtg gcg aca gcc ttg gtg gca 192  
Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala  
50 55 60

gca ccg aaa ctt ctc att ttg gat gag cct acg ttt ggc caa gat ccc 240  
Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro  
65 70 75 80

gag acc ttc aca gag ctg gtg acg atg ttg cgt gaa tta aca gac aac 288  
Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn  
85 90 95

gga atc agc att gtg tca gta acc cat gat cct gat ttc atc gca gcg 336  
Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala  
100 105 110

ctg ggc gat cac cac att gag gtg agc gcg aag tgaacctgct gatcaaaaatt 389  
Leu Gly Asp His His Ile Glu Val Ser Ala Lys  
115 120

aat

392

<210> 110  
 <211> 123  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 110  
 Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly  
     1                    5                    10                    15  
 Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu  
             20                    25                    30  
 Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu  
             35                    40                    45  
 Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala  
             50                    55                    60  
 Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro  
             65                    70                    75                    80  
 Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn  
                     85                    90                    95  
 Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala  
                     100                    105                    110  
 Leu Gly Asp His His Ile Glu Val Ser Ala Lys  
             115                    120

<210> 111  
 <211> 703  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(703)  
 <223> RXN03020

<400> 111  
 cgccgcagca ggactcatcg gtgccgccat ttcactcggc cccatccttc gcgtcgaacc 60  
 acgctccgca ctcatgaacg cataagaaaa ggaacctcac atg act ctc cac gtt 115  
   Met Thr Leu His Val  
   1                    5  
 tca aat ctc aat ctg acc gtc gcc gac gga tcc acc tca cgc acc ctg 163  
 Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser Thr Ser Arg Thr Leu  
                     10                    15                    20  
 ctc aac aac ata cac ttt tgg atg tcc aac cag gcg aag tcg tcg gta 211  
 Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln Ala Lys Ser Ser Val  
                     25                    30                    35  
 tca ccg gcc cat ccg gct ccg gaa aat cca ccc tac tcg ccg tcc tcg 259  
 Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro Tyr Ser Pro Ser Ser  
             40                    45                    50

gct gcc tcc aaa gcg ccc gat tcc ggc acc gcg acg ctc ggc gac atc 307  
 Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala Thr Leu Gly Asp Ile  
     55                    60                    65

gac ctg ctc aac ccc caa aac cga gct gct tta cga cgc aac cac cta 355  
 Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu Arg Arg Asn His Leu  
     70                    75                    80                    85

gga att gtc ttc caa cag cca aac ctg ctc ccc tcg ttg act gtc ctc 403  
 Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro Ser Leu Thr Val Leu  
                     90                    95                    100

gac caa ctg ctg ctc att ccc cgg ctc ggc agg atc ctc ccg ccc agc 451  
 Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg Ile Leu Pro Pro Ser  
             105                    110                    115

cgc agc gca cgc acc caa cac aaa gac aaa gcc ctt tca ctt ctg aac 499  
 Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala Leu Ser Leu Leu Asn  
             120                    125                    130

tcc atc gga ctc ggc gac tta gca aaa cgc aag gtc agc gaa cta tcc 547  
 Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys Val Ser Glu Leu Ser  
     135                    140                    145

ggt gga caa caa gcc cgc gtt aac ttg gcc cgc gcg ctg atg aac tcc 595  
 Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg Ala Leu Met Asn Ser  
     150                    155                    160                    165

ccc aag ctc ctg ctt gtc gat gaa ccc acc gcc gcc ctc gat caa cat 643  
 Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala Ala Leu Asp Gln His  
             170                    175                    180

tcc gcc agc gaa gtc acc gaa cta atc gtc tcg atg gcc cac caa tac 691  
 Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser Met Ala His Gln Tyr  
             185                    190                    195

aac gcc ccc aca 703  
 Asn Ala Pro Thr  
     200

<210> 112

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Met Thr Leu His Val Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser  
     1                    5                    10                    15

Thr Ser Arg Thr Leu Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln  
     20                    25                    30

Ala Lys Ser Ser Val Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro  
     35                    40                    45

Tyr Ser Pro Ser Ser Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala  
     50                    55                    60

Thr Leu Gly Asp Ile Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu

65	70	75	80
Arg Arg Asn His Leu Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro	85	90	95
Ser Leu Thr Val Leu Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg	100	105	110
Ile Leu Pro Pro Ser Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala	115	120	125
Leu Ser Leu Leu Asn Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys	130	135	140
Val Ser Glu Leu Ser Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg	145	150	155
Ala Leu Met Asn Ser Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala	165	170	175
Ala Leu Asp Gln His Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser	180	185	190
Met Ala His Gln Tyr Asn Ala Pro Thr	195	200	

<210> 113  
 <211> 614  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(591)  
 <223> RXN00726

<400> 113

aac gcg ggt cgc ttg tat gtc gat ggc gat ctc att ggc tac cga gag	48
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu	
1 5 10 15	
cgc gat ggc gtg ctg tac gaa atc tct gag aag gac gcc gcc aag cag	96
Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln	
20 25 30	
cgc tcc gat atc ggc atg gtg ttc cag aac ttc aac ctc ttc ccc cac	144
Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His	
35 40 45	
cgc acg gtg atc gag aac atc atc gaa gct ccc atc cac gtg aag aag	192
Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys	
50 55 60	
cag ccc gaa agc aag gcc cgc gca cgt gcc atg gag ctg ctt gag cag	240
Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln	
65 70 75 80	
gtc ggc ctc gcc cac aag gcg gac gcc tac ccc gtc caa ctg tcg ggt	288
Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly	
85 90 95	

ggt cag cag cag cgc gtt gca att gcc cgc gcc gtc gcc atg gag cca 336  
 Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro  
 100 105 110

aag ctc atg ctt ttc gac gaa ccc acc agc gct ttg gac cct gaa ctc 384  
 Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu  
 115 120 125

gtc ggt gaa gtc ctg cga gtg atg aaa cag ctc gcc gac gac ggc atg 432  
 Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met  
 130 135 140

acc atg ctt gtt gtc acc cac gaa atg ggc ttc gcc cac gaa gtc gcc 480  
 Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala  
 145 150 155 160

gac cag gtc gtg ttc atg gcc gat gga gtt gtc gtt gaa gcc gga acc 528  
 Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr  
 165 170 175

ccc gaa caa gtt ctg gac aat cca aag gaa cag cgc acc aaa gac ttc 576  
 Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe  
 180 185 190

ctg tct tct ctg ctc taaccttttc gggtcttaaa aaa 614  
 Leu Ser Ser Leu Leu  
 195

<210> 114

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu  
 1 5 10 15

Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln  
 20 25 30

Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His  
 35 40 45

Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys  
 50 55 60

Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln  
 65 70 75 80

Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly  
 85 90 95

Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro  
 100 105 110

Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu  
 115 120 125

Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met



130	135	140	
Thr Met Leu Val Val	Thr His Glu Met Gly	Phe Ala His Glu Val	Ala
145	150	155	160
Asp Gln Val Val	Phe Met Ala Asp Gly	Val Val Val Glu Ala	Gly Thr
	165	170	175
Pro Glu Gln Val	Leu Asp Asn Pro	Lys Glu Gln Arg Thr	Lys Asp Phe
	180	185	190
Leu Ser Ser Leu Leu			
195			
<210> 115			
<211> 765			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(742)			
<223> RXN02570			
<400> 115			
ccattgttat	gctcattgtg	tttgtggtgg	tcaagtcgct
			acccaagcgc
			accactaggg
			60
cattggttcc	gcagcggggtt	ccggaggacg	tcgcttaaac
			atg aat cct ttg aca
			Met Asn Pro Leu Thr
			1 5
115			
ttg atc att ggc gca ttc agc atg ttg atc gtg gtg ctg ggc gtt aat			163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn			
	10	15	20
aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg			211
Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala			
	25	30	35
atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta			259
Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu			
	40	45	50
tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct			307
Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser			
	55	60	65
tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg			355
Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala			
	70	75	80
85			
ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag			403
Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu			
	90	95	100
ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt			451
Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly			
	105	110	115
tct qca ttg caq atg att ccq caq ggt aaa caq acc ttg gcg ttg gtt			499

Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val  
 120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547  
 Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg  
 135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595  
 Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala  
 150 155 160 165

ggt gcc gcg cga gcg att ccc ttg gag gtc gca ggc ctg gac agg ccg 643  
 Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala Gly Leu Asp Arg Pro  
 170 175 180

ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag 691  
 Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys  
 185 190 195

cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg 739  
 His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp  
 200 205 210

ctc taactcaaat cgtcggaccg tcc 765  
 Leu

<210> 116  
 <211> 214  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 116  
 Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val  
 1 5 10 15

Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile  
 20 25 30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala  
 35 40 45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile  
 50 55 60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr  
 65 70 75 80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala  
 85 90 95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu  
 100 105 110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln  
 115 120 125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val  
 130 135 140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr  
 145 150 155 160  
 His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala  
 165 170 175  
 Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu  
 180 185 190  
 Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val  
 195 200 205  
 Gly Met Ala Trp Trp Leu  
 210

<210> 117  
 <211> 957  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(934)  
 <223> RXN02354

<400> 117  
 gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60  
 ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca 115  
 Met Thr Lys Arg Thr  
 1 5  
 aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163  
 Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp  
 10 15 20  
 gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211  
 Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser  
 25 30 35  
 aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259  
 Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp  
 40 45 50  
 aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307  
 Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala  
 55 60 65  
 gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355  
 Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Ala Ile Ala  
 70 75 80 85  
 gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403  
 Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe  
 90 95 100  
 ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451  
 Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe  
 105 110 115

ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499  
 Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu  
 120 125 130

aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547  
 Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe  
 135 140 145

gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595  
 Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu  
 150 155 160 165

ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc 643  
 Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly  
 170 175 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt 691  
 Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe  
 185 190 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg 739  
 Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu  
 200 205 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc 787  
 Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile  
 215 220 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc 835  
 Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val  
 230 235 240 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883  
 Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu  
 250 255 260

atc ttc caa cgc cgc atc gtc tcc gga ctc acc gca ggt ggc gtg aaa 931  
 Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr Ala Gly Gly Val Lys  
 265 270 275

gcc tagactagat actcatgagt gct 957  
 Ala

&lt;210&gt; 118

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 118

Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val  
 1 5 10 15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr  
 20 25 30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr  
 35 40 45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly

50                      55                      60  
 Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr  
 65                      70                      75                      80  
 Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu  
                     85                      90                      95  
 Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu  
                     100                      105                      110  
 Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln  
                     115                      120                      125  
 Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile  
                     130                      135                      140  
 Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser  
 145                      150                      155                      160  
 Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp  
                     165                      170                      175  
 Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala  
                     180                      185                      190  
 Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp  
                     195                      200                      205  
 Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro  
                     210                      215                      220  
 Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr  
 225                      230                      235                      240  
 Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu  
                     245                      250                      255  
 Ile Ile Met Val Leu Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr  
                     260                      265                      270  
 Ala Gly Gly Val Lys Ala  
                     275

&lt;210&gt; 119

&lt;211&gt; 889

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(889)

&lt;223&gt; FRXA02354

&lt;400&gt; 119

gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60

ttgtaaaggc cgattctgct gtgaaggaag cgcctaagcc atg act aaa cga aca 115

Met Thr Lys Arg Thr

1

5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg	163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp	
10 15 20	
gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc	211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser	
25 30 35	
aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat	259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp	
40 45 50	
aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca	307
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala	
55 60 65	
gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct	355
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala	
70 75 80 85	
gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc	403
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe	
90 95 100	
ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc	451
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe	
105 110 115	
ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc	499
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu	
120 125 130	
aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc	547
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe	
135 140 145	
gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg	595
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu	
150 155 160 165	
ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc	643
Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly	
170 175 180	
caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt	691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe	
185 190 195	
acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg	739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu	
200 205 210	
gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc	787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile	
215 220 225	
gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc	835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val	
230 235 240 245	

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883  
 Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu  
                   250                                  255                                  260

atc ttc 889  
 Ile Phe

<210> 120  
 <211> 263  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 120  
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   1                  5                                  10                                  15  
 Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr  
                   20                                  25                                  30  
 Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr  
                   35                                  40                                  45  
 His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly  
           50                                  55                                  60  
 Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr  
   65                                  70                                  75                                  80  
 Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu  
                   85                                  90                                  95  
 Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu  
                   100                                  105                                  110  
 Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln  
                   115                                  120                                  125  
 Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile  
   130                                  135                                  140  
 Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser  
 145                                  150                                  155                                  160  
 Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp  
                   165                                  170                                  175  
 Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala  
                   180                                  185                                  190  
 Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp  
                   195                                  200                                  205  
 Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro  
   210                                  215                                  220  
 Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr  
 225                                  230                                  235                                  240  
 Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu

245

250

255

Ile Ile Met Val Leu Ile Phe  
260

<210> 121  
<211> 1251  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1228)  
<223> RXN00001

<400> 121  
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gatcggttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115  
Met Ala Thr Val Thr  
1 5  
ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163  
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val  
10 15 20  
aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211  
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val  
25 30 35  
ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259  
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly  
40 45 50  
ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307  
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val  
55 60 65  
acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355  
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn  
70 75 80 85  
tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403  
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala  
90 95 100  
ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451  
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp  
105 110 115  
gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg 499  
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro  
120 125 130  
aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc 547  
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala  
135 140 145  
att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac 595  
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn



150	155	160	165	
ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg				643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu				
	170	175	180	
cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg				691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr				
	185	190	195	
gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac				739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr				
	200	205	210	
ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac				787
Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn				
	215	220	225	
gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc				835
Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr				
	230	235	240	245
ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag				883
Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys				
	250	255	260	
ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc				931
Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg				
	265	270	275	
atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc				979
Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly				
	280	285	290	
gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa				1027
Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu				
	295	300	305	
ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac				1075
Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp				
	310	315	320	325
ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc				1123
Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val				
	330	335	340	
cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca				1171
Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala				
	345	350	355	
cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag				1219
Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys				
	360	365	370	
cgc ctc cct taagcccgcg taccggctac ccc				1251
Arg Leu Pro				
	375			

&lt;210&gt; 122

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 122

Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala  
 1 5 10 15

Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu  
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu  
 35 40 45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile  
 50 55 60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala  
 65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu  
 85 90 95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile  
 100 105 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe  
 115 120 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val  
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp  
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr  
 165 170 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val  
 180 185 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val  
 195 200 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr  
 210 215 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala  
 225 230 235 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly  
 245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro  
 260 265 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu  
 275 280 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu  
 290 295 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu  
 305 310 315 320  
 Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser  
 325 330 335  
 Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly  
 340 345 350  
 Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser  
 355 360 365  
 Ala Ser Thr Gly Lys Arg Leu Pro  
 370 375

<210> 123  
 <211> 1251  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1228)  
 <223> FRXA00001

<400> 123  
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 gatcggttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115  
 Met Ala Thr Val Thr  
 1 5  
 ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163  
 Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val  
 10 15 20  
 aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211  
 Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val  
 25 30 35  
 ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259  
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly  
 40 45 50  
 ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307  
 Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val  
 55 60 65  
 acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355  
 Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn  
 70 75 80 85  
 tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403  
 Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala  
 90 95 100  
 ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451  
 Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp  
 105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg	499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro	
120 125 130	
aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc	547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala	
135 140 145	
att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac	595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn	
150 155 160 165	
ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg	643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu	
170 175 180	
cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg	691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr	
185 190 195	
gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac	739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr	
200 205 210	
ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac	787
Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn	
215 220 225	
gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc	835
Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr	
230 235 240 245	
ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag	883
Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys	
250 255 260	
ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc	931
Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg	
265 270 275	
atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc	979
Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly	
280 285 290	
gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa	1027
Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu	
295 300 305	
ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac	1075
Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp	
310 315 320 325	
ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc	1123
Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val	
330 335 340	
cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca	1171
Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala	
345 350 355	
cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag	1219

Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys  
 360 365 370

cgc ctc cct taagcccgcg taccggctac ccc  
 Arg Leu Pro  
 375

1251

<210> 124  
 <211> 376  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 124  
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 Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu  
 20 25 30  
 Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu  
 35 40 45  
 Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile  
 50 55 60  
 Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala  
 65 70 75 80  
 Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu  
 85 90 95  
 Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile  
 100 105 110  
 Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe  
 115 120 125  
 Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val  
 130 135 140  
 Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp  
 145 150 155 160  
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr  
 165 170 175  
 Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val  
 180 185 190  
 Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val  
 195 200 205  
 Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr  
 210 215 220  
 Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala  
 225 230 235 240  
 Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly  
 245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro  
 260 265 270  
 Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu  
 275 280 285  
 Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu  
 290 295 300  
 Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu  
 305 310 315 320  
 Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser  
 325 330 335  
 Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly  
 340 345 350  
 Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser  
 355 360 365  
 Ala Ser Thr Gly Lys Arg Leu Pro  
 370 375

<210> 125  
 <211> 1119  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1096)  
 <223> RXN02356

<400> 125  
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 Met Ala Thr Val Thr  
 1 5  
 ttc gac aag gtc aca atc cgg tac ccc ggc gcg gag cgc gca aca gtt 163  
 Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val  
 10 15 20  
 cat gag ctt gat tta gat atc gct gat ggc gag ttt ttg gtg ctc gtc 211  
 His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val  
 25 30 35  
 ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg 259  
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly  
 40 45 50  
 ctt gag ggc gtg gag tcg ggt gtg atc aaa att gat ggc aag gat gtc 307  
 Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val  
 55 60 65  
 act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat 355  
 Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn

70	75	80	85	
tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala 90 95 100				403
ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn 105 110 115				451
gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro 120 125 130				499
aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala 135 140 145				547
ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn 150 155 160 165				595
ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu 170 175 180				643
cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val 185 190 195				691
gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu 200 205 210				739
ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn 215 220 225				787
gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro 230 235 240 245				835
gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn 250 255 260				883
gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val 265 270 275				931
gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His 280 285 290				979
cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr 295 300 305				1027
cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu 310 315 320 325				1075

gag tgc ggc gag cgt atc gct tagtttcgga cgtggggagg cgt  
 Glu Ser Gly Glu Arg Ile Ala  
 330

1119

&lt;210&gt; 126

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 126

Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala  
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Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu  
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Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu  
 35 40 45

Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile  
 50 55 60

Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala  
 65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys  
 85 90 95

Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile  
 100 105 110

Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe  
 115 120 125

Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val  
 130 135 140

Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp  
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala  
 165 170 175

Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val  
 180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val  
 195 200 205

Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr  
 210 215 220

Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser  
 225 230 235 240

Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu  
 245 250 255

Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala



260	265	270
Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala		
275	280	285
Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val		
290	295	300
Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala		
305	310	315
His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala		
325	330	

&lt;210&gt; 127

&lt;211&gt; 1369

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1369)

&lt;223&gt; RXN02455

&lt;400&gt; 127

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gctcatcacc	cgccttttta	tcaagaaaga	tgaggacctc	ttg	aag	cgt	ctt	act	115
				Leu	Lys	Arg	Leu	Thr	
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cgc	atc	gca	tcc	atc	agc	atg	gcc	tcc	atg	ctc	gcc	gcc	gca	agt	ctc	163
Arg	Ile	Ala	Ser	Ile	Ser	Met	Ala	Ser	Met	Leu	Ala	Ala	Ala	Ser	Leu	
			10						15					20		

gtc	gcg	tgc	tcc	ggc	tcc	acc	gac	gag	gaa	ggc	gat	gtt	tac	ttc	ctg	211
Val	Ala	Cys	Ser	Gly	Ser	Thr	Asp	Glu	Glu	Gly	Asp	Val	Tyr	Phe	Leu	
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aac	ttc	aag	cct	gaa	cag	gac	gtg	gca	tac	cag	gaa	atc	gca	aag	gcc	259
Asn	Phe	Lys	Pro	Glu	Gln	Asp	Val	Ala	Tyr	Gln	Glu	Ile	Ala	Lys	Ala	
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Tyr	Thr	Glu	Glu	Thr	Gly	Val	Lys	Val	Lys	Val	Val	Thr	Ala	Ala	Ser	
	55					60					65					

ggc	tcc	tat	gag	cag	acc	ctc	aag	gcc	gag	att	ggc	aag	gac	gaa	gcc	355
Gly	Ser	Tyr	Glu	Gln	Thr	Leu	Lys	Ala	Glu	Ile	Gly	Lys	Asp	Glu	Ala	
70				75					80					85		

ccg	act	ctc	ttc	cag	gtc	aat	ggc	cca	gcc	ggc	ttc	atc	act	tg	cag	403
Pro	Thr	Leu	Phe	Gln	Val	Asn	Gly	Pro	Ala	Gly	Phe	Ile	Thr	Trp	Gln	
				90				95						100		

gac	tac	atg	gca	gat	atg	tcg	gac	acc	gag	gta	gct	aag	cag	ctg	acc	451
Asp	Tyr	Met	Ala	Asp	Met	Ser	Asp	Thr	Glu	Val	Ala	Lys	Gln	Leu	Thr	
			105					110					115			

gac	gac	att	cgc	cgc	ctg	acc	acc	gag	gat	ggc	gag	gta	cgt	ggc	gtt	499
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Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly Glu Val Arg Gly Val	
120 125 130	
cgc ttc gcc gtc gag ggc ttc ggc atc atc tac aac gac gag atc ttc	547
Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr Asn Asp Glu Ile Phe	
135 140 145	
gac aag tac atc gcc acg tcc ggc gca aag atc aag tcc acg gat gag	595
Asp Lys Tyr Ile Ala Thr Ser Gly Ala Lys Ile Lys Ser Thr Asp Glu	
150 155 160 165	
atc acg agc tac cag aag ctc aag gaa gtc gcc gag gat atg cag gca	643
Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala Glu Asp Met Gln Ala	
170 175 180	
aag aag gac gag ctc ggt atc gaa ggc gcc ttc gcc tcc acc tcg ctg	691
Lys Lys Asp Glu Leu Gly Ile Glu Gly Ala Phe Ala Ser Thr Ser Leu	
185 190 195	
aca tcc agt gag gac tgg cgt tgg cag acc cac ctg gcc aac gct ccg	739
Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His Leu Ala Asn Ala Pro	
200 205 210	
atc tgg cag gag tac cag gac aag gga gtc gag gac acc aac gag atc	787
Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu Asp Thr Asn Glu Ile	
215 220 225	
gag ttc tcc tac aac aag gag tac aag aac ctt ttc gat ctc tac ctt	835
Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu Phe Asp Leu Tyr Leu	
230 235 240 245	
gag aac tcc acc gta gaa aag tct ctt gcg ccg tct aag acg gtg tct	883
Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro Ser Lys Thr Val Ser	
250 255 260	
gat tcc atg gct gag ttc gca cag ggc aag gcc gct atg gtt cag aac	931
Asp Ser Met Ala Glu Phe Ala Gln Gly Lys Ala Ala Met Val Gln Asn	
265 270 275	
ggt aac tgg gca tgg tcc cag att tcc gag act tct gcc aac gtg gtc	979
Gly Asn Trp Ala Trp Ser Gln Ile Ser Glu Thr Ser Gly Asn Val Val	
280 285 290	
aag gaa gac aag atc aag ttc ctg ccc atg tac atg ggt ctg cca gat	1027
Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr Met Gly Leu Pro Asp	
295 300 305	
gaa gaa aag cac ggc atc aac gtc ggt acc gag aac tat ttg ggc gtg	1075
Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu Asn Tyr Leu Gly Val	
310 315 320 325	
aac tct gag gcc tcc gag gtc gac cag cag gcc acc aag gac ttc gtg	1123
Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala Thr Lys Asp Phe Val	
330 335 340	
gat tgg ctg ttt acc tct gaa gct ggc aag gag cac gtg gtg aag gac	1171
Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu His Val Val Lys Asp	
345 350 355	
ctt ggc ttc atc gca ccg ttc gaa agc tac acc gct gag aac acc ccg	1219
Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr Ala Glu Asn Thr Pro	

360	365	370	
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Asn Asp Pro Leu Ser Glu	Gln Val Ala Glu Ala Ile Ala Asn Lys Asp		
375	380 385		
ctg acc acc tac ccg tgg aac ttc cag tac ttc ccg tcc cag cag ttc	1315		
Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe Pro Ser Gln Gln Phe			
390	395 400 405		
aag gat gac ttc ggc cag gat ctg tgc cag tac gcc tcc gga aag ctg	1363		
Lys Asp Asp Phe Gly Gln Asp Leu Ser Gln Tyr Ala Ser Gly Lys Leu			
410	415 420		
aag tgg	1369		
Lys Trp			

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45  
 Glu Ile Ala Lys Ala Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val  
 50 55 60  
 Val Thr Ala Ala Ser Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile  
 65 70 75 80  
 Gly Lys Asp Glu Ala Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly  
 85 90 95  
 Phe Ile Thr Trp Gln Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val  
 100 105 110  
 Ala Lys Gln Leu Thr Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly  
 115 120 125  
 Glu Val Arg Gly Val Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr  
 130 135 140  
 Asn Asp Glu Ile Phe Asp Lys Tyr Ile Ala Thr Ser Gly Ala Lys Ile  
 145 150 155 160  
 Lys Ser Thr Asp Glu Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala  
 165 170 175  
 Glu Asp Met Gln Ala Lys Lys Asp Glu Leu Gly Ile Glu Gly Ala Phe  
 180 185 190

Ala Ser Thr Ser Leu Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His  
 195 200 205

Leu Ala Asn Ala Pro Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu  
 210 215 220

Asp Thr Asn Glu Ile Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu  
 225 230 235 240

Phe Asp Leu Tyr Leu Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro  
 245 250 255

Ser Lys Thr Val Ser Asp Ser Met Ala Glu Phe Ala Gln Gly Lys Ala  
 260 265 270

Ala Met Val Gln Asn Gly Asn Trp Ala Trp Ser Gln Ile Ser Glu Thr  
 275 280 285

Ser Gly Asn Val Val Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr  
 290 295 300

Met Gly Leu Pro Asp Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu  
 305 310 315 320

Asn Tyr Leu Gly Val Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala  
 325 330 335

Thr Lys Asp Phe Val Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu  
 340 345 350

His Val Val Lys Asp Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr  
 355 360 365

Ala Glu Asn Thr Pro Asn Asp Pro Leu Ser Glu Gln Val Ala Glu Ala  
 370 375 380

Ile Ala Asn Lys Asp Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe  
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Ala Ser Gly Lys Leu Lys Trp  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1537)  
 <223> RXN02795

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 Val Leu Lys Val Ser

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gat	tta	acg	gtt	ggc	aac	aat	ttt	gtc	cac	aac	gtc	tcc	ttc	gag	gtc	163	
Asp	Leu	Thr	Val	Gly	Asn	Asn	Phe	Val	His	Asn	Val	Ser	Phe	Glu	Val		
				10					15					20			
aac	ccc	ggc	gaa	cgc	gtc	ggc	atc	atc	ggc	gag	tcc	ggc	tca	ggc	aaa	211	
Asn	Pro	Gly	Glu	Arg	Val	Gly	Ile	Ile	Gly	Glu	Ser	Gly	Ser	Gly	Lys		
				25					30					35			
tca	ctc	acc	gcg	cta	tcc	atc	atg	ggg	tta	act	gac	ctg	ccg	acc	acc	259	
Ser	Leu	Thr	Ala	Leu	Ser	Ile	Met	Gly	Leu	Thr	Asp	Leu	Pro	Thr	Thr		
				40					45					50			
ggc	cag	atc	acc	ttc	aac	ggc	aaa	ccc	tcc	gct	aca	ttc	cgt	ggc	acc	307	
Gly	Gln	Ile	Thr	Phe	Asn	Gly	Lys	Pro	Ser	Ala	Thr	Phe	Arg	Gly	Thr		
				55					60					65			
cgc	atc	gcc	atg	gtt	ttc	caa	gaa	cca	atg	agc	gca	ctc	aac	ccg	ctc	355	
Arg	Ile	Ala	Met	Val	Phe	Gln	Glu	Pro	Met	Ser	Ala	Leu	Asn	Pro	Leu		
				70					75					80			
atg	cgc	atc	ggc	cgc	caa	atc	gaa	gaa	atg	atg	acc	ctg	cac	ggg	gca	403	
Met	Arg	Ile	Gly	Arg	Gln	Ile	Glu	Glu	Met	Met	Thr	Leu	His	Gly	Ala		
				90					95					100			
agc	aaa	aaa	gac	gcg	cgg	gcg	cgc	tta	aaa	agc	ttg	ctt	atc	gac	gtc	451	
Ser	Lys	Lys	Asp	Ala	Arg	Ala	Arg	Leu	Lys	Ser	Leu	Leu	Ile	Asp	Val		
				105					110					115			
tcc	ctc	ccc	gaa	cgc	acc	gct	tcg	gcc	tac	cca	cac	gaa	ctt	tca	ggc	499	
Ser	Leu	Pro	Glu	Arg	Thr	Ala	Ser	Ala	Tyr	Pro	His	Glu	Leu	Ser	Gly		
				120					125					130			
ggg	caa	cgc	caa	cgc	gca	cta	atc	gca	atg	gcg	ctg	gcc	aat	gat	cct	547	
Gly	Gln	Arg	Gln	Arg	Ala	Leu	Ile	Ala	Met	Ala	Leu	Ala	Asn	Asp	Pro		
				135					140					145			
gac	ctg	ttg	atc	tgc	gat	gaa	ccc	acc	acg	gct	ttg	gat	gtg	gtt	gtg	595	
Asp	Leu	Leu	Ile	Cys	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Val	Val		
				150					155					160			
caa	aaa	caa	atc	gtc	gat	ctg	ctg	ctg	cgt	ctc	acc	aaa	gaa	cgt	ggc	643	
Gln	Lys	Gln	Ile	Val	Asp	Leu	Leu	Leu	Arg	Leu	Thr	Lys	Glu	Arg	Gly		
				170					175					180			
acc	gct	tta	ttg	ttc	atc	acc	cac	gat	ctt	gga	ctc	atc	gcg	cgc	acc	691	
Thr	Ala	Leu	Leu	Phe	Ile	Thr	His	Asp	Leu	Gly	Leu	Ile	Ala	Arg	Thr		
				185					190					195			
tgc	gaa	cgc	tta	ttg	gtg	atg	aaa	tcc	ggc	gaa	acc	gta	gaa	cgc	ggc	739	
Cys	Glu	Arg	Leu	Leu	Val	Met	Lys	Ser	Gly	Glu	Thr	Val	Glu	Arg	Gly		
				200					205					210			
gac	acc	gag	gca	att	ctt	cgc	tcc	ccc	gcc	cat	tcg	tat	acc	caa	cag	787	
Asp	Thr	Glu	Ala	Ile	Leu	Arg	Ser	Pro	Ala	His	Ser	Tyr	Thr	Gln	Gln		
				215					220					225			
ctc	ctt	gat	gct	tca	atc	ctt	gac	cag	cca	gaa	atc	gcc	tca	gat	tct	835	
Leu	Leu	Asp	Ala	Ser	Ile	Leu	Asp	Gln	Pro	Glu	Ile	Ala	Ser	Asp	Ser		
				230					235					240			

ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa agc ttt aaa	883
Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys Ser Phe Lys	
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Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg Lys Gly Asp	
265 270 275	
ctg ctt gga ata gtc ggc gga tca ggt tcc ggc aaa acg act ctg ctg	979
Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr Thr Leu Leu	
280 285 290	
aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc gtt gcg gta	1027
Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr Val Ala Val	
295 300 305	
acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca agc ctc aac	1075
Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser Ser Leu Asn	
310 315 320 325	
cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg ctt ggt tgg	1123
Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu Leu Gly Trp	
330 335 340	
aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc acc caa gtg	1171
Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile Thr Gln Val	
345 350 355	
gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa ttc tcc gga	1219
Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu Phe Ser Gly	
360 365 370	
gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc atc aaa cca	1267
Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala Ile Lys Pro	
375 380 385	
gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat gtg tcc gta	1315
Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp Val Ser Val	
390 395 400 405	
cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa gaa tac ggc	1363
Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu Glu Tyr Gly	
410 415 420	
atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg aga cac ctg	1411
Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val Arg His Leu	
425 430 435	
tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt gag caa ggg	1459
Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu Glu Gln Gly	
440 445 450	
ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac acc aag gag	1507
Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr Thr Lys Glu	
455 460 465	
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Leu Leu Asp Ala Val Pro Arg Leu Ser Leu	
470 475	

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 130

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			20					25					30		
Ser	Gly	Ser	Gly	Lys	Ser	Leu	Thr	Ala	Leu	Ser	Ile	Met	Gly	Leu	Thr
		35					40					45			
Asp	Leu	Pro	Thr	Thr	Gly	Gln	Ile	Thr	Phe	Asn	Gly	Lys	Pro	Ser	Ala
	50					55					60				
Thr	Phe	Arg	Gly	Thr	Arg	Ile	Ala	Met	Val	Phe	Gln	Glu	Pro	Met	Ser
65					70					75					80
Ala	Leu	Asn	Pro	Leu	Met	Arg	Ile	Gly	Arg	Gln	Ile	Glu	Glu	Met	Met
				85					90					95	
Thr	Leu	His	Gly	Ala	Ser	Lys	Lys	Asp	Ala	Arg	Ala	Arg	Leu	Lys	Ser
			100					105					110		
Leu	Leu	Ile	Asp	Val	Ser	Leu	Pro	Glu	Arg	Thr	Ala	Ser	Ala	Tyr	Pro
		115					120					125			
His	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ala	Leu	Ile	Ala	Met	Ala
	130					135					140				
Leu	Ala	Asn	Asp	Pro	Asp	Leu	Leu	Ile	Cys	Asp	Glu	Pro	Thr	Thr	Ala
145					150					155					160
Leu	Asp	Val	Val	Val	Gln	Lys	Gln	Ile	Val	Asp	Leu	Leu	Leu	Arg	Leu
			165					170						175	
Thr	Lys	Glu	Arg	Gly	Thr	Ala	Leu	Leu	Phe	Ile	Thr	His	Asp	Leu	Gly
		180						185					190		
Leu	Ile	Ala	Arg	Thr	Cys	Glu	Arg	Leu	Leu	Val	Met	Lys	Ser	Gly	Glu
	195						200					205			
Thr	Val	Glu	Arg	Gly	Asp	Thr	Glu	Ala	Ile	Leu	Arg	Ser	Pro	Ala	His
	210					215					220				
Ser	Tyr	Thr	Gln	Gln	Leu	Leu	Asp	Ala	Ser	Ile	Leu	Asp	Gln	Pro	Glu
225					230					235					240
Ile	Ala	Ser	Asp	Ser	Gly	Ala	Pro	Val	Val	Ile	Asp	Val	Glu	Glu	Ala
				245					250					255	
Ser	Lys	Ser	Phe	Lys	Glu	Thr	Thr	Ala	Leu	His	Lys	Val	Ser	Leu	Ala
			260					265					270		
Val	Arg	Lys	Gly	Asp	Leu	Leu	Gly	Ile	Val	Gly	Gly	Ser	Gly	Ser	Gly
		275					280					285			

Lys Thr Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr  
 290 295 300  
 Gly Thr Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro  
 305 310 315 320  
 Gln Ser Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu  
 325 330 335  
 Pro Leu Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu  
 340 345 350  
 Val Ile Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro  
 355 360 365  
 His Glu Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala  
 370 375 380  
 Leu Ala Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala  
 385 390 395 400  
 Leu Asp Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu  
 405 410 415  
 Val Glu Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala  
 420 425 430  
 Val Val Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg  
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 Val Leu Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr  
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 Glu Tyr Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu  
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 ctt tca ggc ggg caa cgc caa cgc gca cta atc gca atg gcg ctg gcc 96  
 Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala  
 20 25 30  
 aat gat cct gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat 144  
 Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp  
 35 40 45  
 gtg gtt gtg caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa 192



Val	Val	Val	Gln	Lys	Gln	Ile	Val	Asp	Leu	Leu	Leu	Arg	Leu	Thr	Lys	
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gaa	cgt	ggc	acc	gct	tta	ttg	ttc	atc	acc	cac	gat	ctt	gga	ctc	atc	240
Glu	Arg	Gly	Thr	Ala	Leu	Leu	Phe	Ile	Thr	His	Asp	Leu	Gly	Leu	Ile	
65					70				75						80	
gcg	cgc	acc	tgc	gaa	cgc	tta	ttg	gtg	atg	aaa	tcc	ggc	gaa	acc	gta	288
Ala	Arg	Thr	Cys	Glu	Arg	Leu	Leu	Val	Met	Lys	Ser	Gly	Glu	Thr	Val	
				85					90					95		
gaa	cgc	ggc	gac	acc	gag	gca	att	ctt	cgc	tcc	ccc	gcc	cat	tcg	tat	336
Glu	Arg	Gly	Asp	Thr	Glu	Ala	Ile	Leu	Arg	Ser	Pro	Ala	His	Ser	Tyr	
			100					105					110			
acc	caa	cag	ctc	ctt	gat	gct	tca	atc	ctt	gac	cag	cca	gaa	atc	gcc	384
Thr	Gln	Gln	Leu	Leu	Asp	Ala	Ser	Ile	Leu	Asp	Gln	Pro	Glu	Ile	Ala	
			115					120				125				
tca	gat	tct	ggc	gcg	ccg	gta	gtg	att	gat	gtg	gag	gag	gcg	tcg	aaa	432
Ser	Asp	Ser	Gly	Ala	Pro	Val	Val	Ile	Asp	Val	Glu	Glu	Ala	Ser	Lys	
	130					135					140					
agc	ttt	aaa	gaa	acc	acc	gcc	ctc	cac	aag	gtt	tca	ttg	gcg	gtg	cgc	480
Ser	Phe	Lys	Glu	Thr	Thr	Ala	Leu	His	Lys	Val	Ser	Leu	Ala	Val	Arg	
145					150				155						160	
aaa	ggt	gac	ctg	ctt	gga	ata	gtc	ggc	gga	tca	ggt	tcc	ggc	aaa	acg	528
Lys	Gly	Asp	Leu	Leu	Gly	Ile	Val	Gly	Gly	Ser	Gly	Ser	Gly	Lys	Thr	
				165				170						175		
act	ctg	ctg	aag	ctc	atc	gcc	ggt	ttg	gat	aag	ccc	aca	acc	ggt	acc	576
Thr	Leu	Leu	Lys	Leu	Ile	Ala	Gly	Leu	Asp	Lys	Pro	Thr	Thr	Gly	Thr	
			180					185					190			
gtt	gcg	gta	acc	ggt	ggt	gtg	cag	atg	gtg	ttt	cag	gat	ccc	caa	tca	624
Val	Ala	Val	Thr	Gly	Gly	Val	Gln	Met	Val	Phe	Gln	Asp	Pro	Gln	Ser	
		195					200					205				
agc	ctc	aac	cca	cgg	atg	aaa	atc	aaa	gac	att	gtc	gcc	gaa	cca	ctg	672
Ser	Leu	Asn	Pro	Arg	Met	Lys	Ile	Lys	Asp	Ile	Val	Ala	Glu	Pro	Leu	
	210					215					220					
ctt	ggt	tgg	aac	gcg	gcg	gag	aaa	acc	aca	cgg	gtt	gcg	gaa	gtc	atc	720
Leu	Gly	Trp	Asn	Ala	Ala	Glu	Lys	Thr	Thr	Arg	Val	Ala	Glu	Val	Ile	
225					230					235					240	
acc	caa	gtg	gga	ctg	agc	ccc	gat	gtc	tta	gat	cgc	tac	ccc	cac	gaa	768
Thr	Gln	Val	Gly	Leu	Ser	Pro	Asp	Val	Leu	Asp	Arg	Tyr	Pro	His	Glu	
				245				250						255		
ttc	tcc	gga	gga	cag	cgc	caa	cga	atc	tcc	atc	gcc	aga	gcc	ctc	gcc	816
Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ser	Ile	Ala	Arg	Ala	Leu	Ala	
			260					265					270			
atc	aaa	cca	gcg	atc	ctg	ctt	gcc	gac	gaa	cct	gtc	tcc	gcc	ctc	gat	864
Ile	Lys	Pro	Ala	Ile	Leu	Leu	Ala	Asp	Glu	Pro	Val	Ser	Ala	Leu	Asp	
		275					280					285				
gtg	tcc	gta	cgt	aaa	caa	gta	ctg	gat	ctt	ctc	caa	caa	ctc	gtc	gaa	912
Val	Ser	Val	Arg	Lys	Gln	Val	Leu	Asp	Leu	Leu	Gln	Gln	Leu	Val	Glu	

290 295 300

gaa tac ggc atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg 960  
 Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val  
 305 310 315 320

aga cac ctg tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt 1008  
 Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu  
 325 330 335

gag caa ggg ccc atc gat tgc gtt tat gat cac cca cag acc gaa tac 1056  
 Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr  
 340 345 350

acc aag gag ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg 1105  
 Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu  
 355 360 365

cagatgacaa cgc 1118

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Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp  
 35 40 45

Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys  
 50 55 60

Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile  
 65 70 75 80

Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val  
 85 90 95

Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr  
 100 105 110

Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala  
 115 120 125

Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys  
 130 135 140

Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg  
 145 150 155 160

Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr  
 165 170 175

Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr

180	185	190
Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser		
195	200	205
Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu		
210	215	220
Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile		
225	230	235
Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu		
245	250	255
Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala		
260	265	270
Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp		
275	280	285
Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu		
290	295	300
Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val		
305	310	315
Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu		
325	330	335
Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr		
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Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu		
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 Met Thr Thr Asn Ile  
 1 5  
 cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag 163  
 Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys  
 10 15 20  
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 Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val  
 25 30 35

cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg	259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val	
40 45 50	
ggt gaa tcc ggt tca ggt aaa tct acc acg gca atg tct atc atc ggt	307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly	
55 60 65	
ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat	355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp	
70 75 80 85	
ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc	403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg	
90 95 100	
ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac	451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn	
105 110 115	
ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac	499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn	
120 125 130	
cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg	547
His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu	
135 140 145	
gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca	595
Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro	
150 155 160 165	
cat gag ttc tct ggc ggt atg cgc cag cgc gca ctg atc gcc att ggt	643
His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala Leu Ile Ala Ile Gly	
170 175 180	
ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg	691
Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala	
185 190 195	
ctg gat gtc acc gtg cag cgc caa atc ctt gat cac ctt gaa aca ctg	739
Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp His Leu Glu Thr Leu	
200 205 210	
acc aag gat ctc ggc acc gca gtg cta ttt att acc cac gac ttg ggc	787
Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile Thr His Asp Leu Gly	
215 220 225	
ctt gcc gct gag cgc gcg gag cac ctc gtg gtg atg cac cgc gga cgc	835
Leu Ala Ala Glu Arg Ala Glu His Leu Val Val Met His Arg Gly Arg	
230 235 240 245	
atc gtg gag tcc ggg cca tca ttg aag att ctg cgc aat cca cag cac	883
Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu Arg Asn Pro Gln His	
250 255 260	
cca tat acc caa cgc ttg gtt aag gct gcg ccg tct ctg gct tct gca	931
Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro Ser Leu Ala Ser Ala	
265 270 275	
cgt att caa agt gcg cag gaa caa ggc att gaa tct gca gaa ctg ctc	979

Arg	Ile	Gln	Ser	Ala	Gln	Glu	Gln	Gly	Ile	Glu	Ser	Ala	Glu	Leu	Leu		
	280						285					290					
tct	gca	acg	gcc	gtt	gct	gag	ggc	act	att	cca	gag	atg	gaa	gaa	aaa	1027	
Ser	Ala	Thr	Ala	Val	Ala	Glu	Gly	Thr	Ile	Pro	Glu	Met	Glu	Glu	Lys		
	295					300				305							
gtt	atc	gag	gtg	aaa	aac	ctc	acc	cgc	gaa	ttt	gat	atc	cgc	ggg	gcc	1075	
Val	Ile	Glu	Val	Lys	Asn	Leu	Thr	Arg	Glu	Phe	Asp	Ile	Arg	Gly	Ala		
310					315				320					325			
cgt	ggc	gat	aag	aag	aag	ctg	aag	gcc	gtt	gat	gat	gtg	tcc	ttc	ttc	1123	
Arg	Gly	Asp	Lys	Lys	Lys	Leu	Lys	Ala	Val	Asp	Asp	Val	Ser	Phe	Phe		
			330						335					340			
gta	cgt	aaa	ggc	acc	acc	acc	gca	ctt	gtg	ggg	gaa	tcc	ggg	tcg	ggg	1171	
Val	Arg	Lys	Gly	Thr	Thr	Thr	Ala	Leu	Val	Gly	Glu	Ser	Gly	Ser	Gly		
			345					350					355				
aaa	tcc	acc	gtg	gcc	aac	atg	gtg	ctc	aac	ctt	ctc	gag	cca	acc	agc	1219	
Lys	Ser	Thr	Val	Ala	Asn	Met	Val	Leu	Asn	Leu	Leu	Glu	Pro	Thr	Ser		
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gga	gag	gtg	ctc	tac	aac	ggc	acc	gat	ctt	acg	tcc	ttg	agc	cac	aag	1267	
Gly	Glu	Val	Leu	Tyr	Asn	Gly	Thr	Asp	Leu	Thr	Ser	Leu	Ser	His	Lys		
	375					380					385						
gaa	atc	ttc	caa	atg	cga	cgc	aaa	ctg	cag	gtg	gtg	ttc	cag	aac	ccc	1315	
Glu	Ile	Phe	Gln	Met	Arg	Arg	Lys	Leu	Gln	Val	Val	Phe	Gln	Asn	Pro		
390					395				400						405		
tac	ggc	tcg	ctt	gat	ccg	atg	tac	tcc	atc	tac	cgg	tgt	att	gag	gaa	1363	
Tyr	Gly	Ser	Leu	Asp	Pro	Met	Tyr	Ser	Ile	Tyr	Arg	Cys	Ile	Glu	Glu		
				410					415					420			
ccg	ctg	acc	atc	cac	aag	gtt	ggg	gga	gac	cgc	aag	gca	cgc	gaa	gct	1411	
Pro	Leu	Thr	Ile	His	Lys	Val	Gly	Gly	Asp	Arg	Lys	Ala	Arg	Glu	Ala		
			425					430					435				
cgc	gtc	gct	gaa	ctt	ctc	gat	atg	gtg	tcc	atg	ccc	agg	tcc	acc	atg	1459	
Arg	Val	Ala	Glu	Leu	Leu	Asp	Met	Val	Ser	Met	Pro	Arg	Ser	Thr	Met		
		440					445					450					
cgc	cgc	tac	ccc	aac	gag	ctt	tcc	ggg	ggc	caa	cgt	cag	cgc	atc	gcc	1507	
Arg	Arg	Tyr	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala		
	455					460					465						
atc	gcc	cgt	gca	ttg	gca	ctg	aat	cca	gaa	gtg	atc	gtg	ttg	gat	gaa	1555	
Ile	Ala	Arg	Ala	Leu	Ala	Leu	Asn	Pro	Glu	Val	Ile	Val	Leu	Asp	Glu		
470					475				480					485			
gcg	gtt	tcc	gct	ttg	gac	gtg	ttg	gtt	cag	aac	cag	atc	ctc	acc	ctg	1603	
Ala	Val	Ser	Ala	Leu	Asp	Val	Leu	Val	Gln	Asn	Gln	Ile	Leu	Thr	Leu		
				490					495					500			
ctt	gca	gaa	ctt	cag	cag	gaa	ctg	aag	ctc	acc	tat	ttg	ttc	atc	acc	1651	
Leu	Ala	Glu	Leu	Gln	Gln	Glu	Leu	Lys	Leu	Thr	Tyr	Leu	Phe	Ile	Thr		
			505					510					515				
cac	gac	ttg	gcc	gtt	gtt	cga	caa	acc	gcc	gac	gat	gtt	gtg	gtg	atg	1699	
His	Asp	Leu	Ala	Val	Val	Arg	Gln	Thr	Ala	Asp	Asp	Val	Val	Val	Met		

520                      525                      530

caa aag gga cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac 1747  
 Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn  
 535                      540                      545

gat cct cag cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt 1795  
 Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly  
 550                      555                      560                      565

ctg gga atc gag ttg ggt act gga gaa aac ctg gtt taaccgcac 1841  
 Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu Val  
 570                      575

agcctcacta aac 1854

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 <213> Corynebacterium glutamicum

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 20                      25                      30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln  
 35                      40                      45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala  
 50                      55                      60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly  
 65                      70                      75                      80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln  
 85                      90                      95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro  
 100                      105                      110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu  
 115                      120                      125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg  
 130                      135                      140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg  
 145                      150                      155                      160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala  
 165                      170                      175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp  
 180                      185                      190

Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp  
 195                      200                      205

His Leu Glu Thr Leu Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile  
 210 215 220  
 Thr His Asp Leu Gly Leu Ala Ala Glu Arg Ala Glu His Leu Val Val  
 225 230 235 240  
 Met His Arg Gly Arg Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu  
 245 250 255  
 Arg Asn Pro Gln His Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro  
 260 265 270  
 Ser Leu Ala Ser Ala Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu  
 275 280 285  
 Ser Ala Glu Leu Leu Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro  
 290 295 300  
 Glu Met Glu Glu Lys Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe  
 305 310 315 320  
 Asp Ile Arg Gly Ala Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp  
 325 330 335  
 Asp Val Ser Phe Phe Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly  
 340 345 350  
 Glu Ser Gly Ser Gly Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu  
 355 360 365  
 Leu Glu Pro Thr Ser Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr  
 370 375 380  
 Ser Leu Ser His Lys Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val  
 385 390 395 400  
 Val Phe Gln Asn Pro Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr  
 405 410 415  
 Arg Cys Ile Glu Glu Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg  
 420 425 430  
 Lys Ala Arg Glu Ala Arg Val Ala Glu Leu Leu Asp Met Val Ser Met  
 435 440 445  
 Pro Arg Ser Thr Met Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln  
 450 455 460  
 Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val  
 465 470 475 480  
 Ile Val Leu Asp Glu Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn  
 485 490 495  
 Gln Ile Leu Thr Leu Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr  
 500 505 510  
 Tyr Leu Phe Ile Thr His Asp Leu Ala Val Val Arg Gln Thr Ala Asp  
 515 520 525

Asp Val Val Val Met Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr  
530 535 540

Asp Asp Ile Phe Asn Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile  
545 550 555 560

Asn Ala Val Pro Gly Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu  
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Val

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<211> 691

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(691)

<223> FRXA00761

<400> 135

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Met Thr Thr Asn Ile  
1 5

cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctg gag ctg aag 163  
Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys  
10 15 20

gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc 211  
Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val  
25 30 35

cgt ggc gca aac ctg acc att tat cct ggc caa tct gtt gcc atc gtg 259  
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val  
40 45 50

ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt 307  
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly  
55 60 65

ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat 355  
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp  
70 75 80 85

ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc 403  
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg  
90 95 100

ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac 451  
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn  
105 110 115

ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctg cga gcc aac 499  
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn  
120 125 130



cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg 547  
 His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu  
 135 140 145

gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca 595  
 Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro  
 150 155 160 165

cat gag ttc tct ggc ggt atg cgc cac cgc gca ctg atc gcc att ggt 643  
 His Glu Phe Ser Gly Gly Met Arg His Arg Ala Leu Ile Ala Ile Gly  
 170 175 180

ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg 691  
 Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala  
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<213> Corynebacterium glutamicum

<400> 136

Met Thr Thr Asn Ile Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro  
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Leu Leu Glu Leu Lys Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly  
 20 25 30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln  
 35 40 45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala  
 50 55 60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly  
 65 70 75 80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln  
 85 90 95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro  
 100 105 110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu  
 115 120 125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg  
 130 135 140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg  
 145 150 155 160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg His Arg Ala  
 165 170 175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp  
 180 185 190

Glu Pro Thr Ser Ala

195

<210> 137  
 <211> 626  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(603)  
 <223> FRXA01939

<400> 137  
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 Ser Thr Ser Gly Thr Asp Leu Thr Ser Leu Ser His Lys Glu Ile Phe  
 1 5 10 15

caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc tac ggc tcg 96  
 Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser  
 20 25 30

ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa ccg ctg acc 144  
 Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr  
 35 40 45

atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct cgc gtc gtt 192  
 Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val  
 50 55 60

gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg cgc cgc tac 240  
 Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr  
 65 70 75 80

ccc aac gag ctt tcc ggt ggc caa cgt cag cgc atc gcc atc gcc cgt 288  
 Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg  
 85 90 95

gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa gcg gtt tcc 336  
 Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser  
 100 105 110

gct ttg gac gtg ttg gtt cag aac cag atc ctc acc ctg ctt gca gaa 384  
 Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu  
 115 120 125

ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc cac gac ttg 432  
 Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu  
 130 135 140

gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg caa aag gga 480  
 Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly  
 145 150 155 160

cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac gat cct cag 528  
 Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln  
 165 170 175

cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt ctg gga atc 576  
 Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile  
 180 185 190

gag ttg ggt act gga gaa aac ctg gtt taacccgcac agcctcacta aac 626  
 Glu Leu Gly Thr Gly Glu Asn Leu Val  
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<210> 138  
 <211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 138  
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 Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser  
           20                  25                  30  
 Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr  
           35                  40                  45  
 Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val  
           50                  55                  60  
 Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr  
   65                  70                  75                  80  
 Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg  
           85                  90                  95  
 Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser  
           100                  105                  110  
 Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu  
           115                  120                  125  
 Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu  
           130                  135                  140  
 Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly  
   145                  150                  155                  160  
 Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln  
           165                  170                  175  
 Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile  
           180                  185                  190  
 Glu Leu Gly Thr Gly Glu Asn Leu Val  
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<210> 139  
 <211> 1047  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1024)  
 <223> RXN00759

<400> 139  
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accataatcc attccccagc aagcaaggac acccacgctc atg ctt cgt tac gtc 115  
Met Leu Arg Tyr Val  
1 5  
ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163  
Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu  
10 15 20  
ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca 211  
Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala  
25 30 35  
ttg gga ggt gac cgc gcc cta acc gag gct gcg gcc gag aaa atc cgt 259  
Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg  
40 45 50  
caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac 307  
Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr  
55 60 65  
atc aag gcc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag 355  
Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln  
70 75 80 85  
cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc 403  
Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu  
90 95 100  
gcc atc atg gcc ctg ctg ttt gaa tca atc ctc gcc att atc ttt ggt 451  
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly  
105 110 115  
gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg 499  
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu  
120 125 130  
gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc 547  
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe  
135 140 145  
gtg ctg cag ttc tta gtc gcc gtg aaa tgg gcc tta ctg ccc gtc acc 595  
Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly Leu Leu Pro Val Thr  
150 155 160 165  
gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta 643  
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val  
170 175 180  
ctg ggt gca gta tgc ttc gcc tac gtt ctt cgc ctc acc aga caa tcc 691  
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser  
185 190 195  
gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa 739  
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys  
200 205 210  
ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca 787

Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser  
 215 220 225  
 ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg 835  
 Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met  
 230 235 240 245  
 ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt 883  
 Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly  
 250 255 260  
 gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc 931  
 Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val  
 265 270 275  
 tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979  
 Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu  
 280 285 290  
 gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024  
 Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala  
 295 300 305  
 taataatgaa ttccacacaa acc 1047

<210> 140  
 <211> 308  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 140  
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 Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly  
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 Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala  
 35 40 45  
 Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val  
 50 55 60  
 Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr  
 65 70 75 80  
 Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro  
 85 90 95  
 Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu  
 100 105 110  
 Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe  
 115 120 125  
 Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr  
 130 135 140  
 Phe Val Ile Gly Phe Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly  
 145 150 155 160

Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile  
 165 170 175  
 Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg  
 180 185 190  
 Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg  
 195 200 205  
 Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His  
 210 215 220  
 Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp  
 225 230 235 240  
 Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly  
 245 250 255  
 Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu  
 260 265 270  
 Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile  
 275 280 285  
 Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg  
 290 295 300  
 Ile Arg Tyr Ala  
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<210> 141  
 <211> 1047  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1024)  
 <223> FRXA00759

<220>  
 <223> All occurrences of n = any nucleotide

<220>  
 <223> All occurrences of Xaa = any amino acid

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accataatcc attccccagc aagcaaggac acccaagctc atg ctt cgt tac gtc 115  
 Met Leu Arg Tyr Val  
 1 5

ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163  
 Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu  
 10 15 20

ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca 211  
 Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala

25	30	35	
ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt			259
Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg			
40	45	50	
caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac			307
Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr			
55	60	65	
atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag			355
Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln			
70	75	80	85
cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc			403
Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu			
90	95	100	
gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt			451
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly			
105	110	115	
gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg			499
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu			
120	125	130	
gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc			547
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe			
135	140	145	
gtg ctg cag ttc tta ntc ggc gtg aaa tgg ggc tta ctg ccc gtc acc			595
Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly Leu Leu Pro Val Thr			
150	155	160	165
gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta			643
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val			
170	175	180	
ctg ggt gca gta tgc ttc gcc tac gtt ctt cgc ctc acc aga caa tcc			691
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser			
185	190	195	
gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa			739
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys			
200	205	210	
ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca			787
Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser			
215	220	225	
ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg			835
Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met			
230	235	240	245
ggg gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt			883
Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly			
250	255	260	
gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc			931
Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val			
265	270	275	

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979  
 Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu  
 280 285 290  
 gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024  
 Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala  
 295 300 305  
 taataatgaa ttccacacaa acc 1047

<210> 142  
 <211> 308  
 <212> PRT  
 <213> Corynebacterium glutamicum

<220>  
 <223> All occurrences of Xaa = any amino acid

<400> 142  
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 Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly  
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 Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala  
 35 40 45  
 Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val  
 50 55 60  
 Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr  
 65 70 75 80  
 Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro  
 85 90 95  
 Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu  
 100 105 110  
 Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe  
 115 120 125  
 Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr  
 130 135 140  
 Phe Val Ile Gly Phe Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly  
 145 150 155 160  
 Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile  
 165 170 175  
 Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg  
 180 185 190  
 Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg  
 195 200 205  
 Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His



210 215 220  
 Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp  
 225 230 235 240  
 Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly  
 245 250 255  
 Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu  
 260 265 270  
 Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile  
 275 280 285  
 Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg  
 290 295 300  
 Ile Arg Tyr Ala  
 305

<210> 143  
 <211> 912  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(889)  
 <223> RXN00431

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 Met Val Ser Ile Asp  
 1 5  
 aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163  
 Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe Asp Ala Lys Ser Arg  
 10 15 20  
 tcc atg aag aaa gcc ttc ctc ggc gca gcc ggc gga gca atc ggg cgc 211  
 Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly Gly Ala Ile Gly Arg  
 25 30 35  
 aat caa gac aac gtc gta gtc gtc gaa gcg ctg aag aac gtc aac ctg 259  
 Asn Gln Asp Asn Val Val Val Glu Ala Leu Lys Asn Val Asn Leu  
 40 45 50  
 cac ttg cgc gaa ggt gac cgg gtc gga ctc gtc ggc cac aac ggc gcc 307  
 His Leu Arg Glu Gly Asp Arg Val Gly Leu Val Gly His Asn Gly Ala  
 55 60 65  
 ggc aaa tcc acc ctc ctg cga ctc ctc tcc ggc atc tac gaa ccc acc 355  
 Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr  
 70 75 80 85  
 cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc 403  
 Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu  
 90 95 100

ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc 451  
 Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile  
 105 110 115  
  
 cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg 499  
 Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met  
 120 125 130  
  
 gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct 547  
 Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro  
 135 140 145  
  
 ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg 595  
 Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val  
 150 155 160 165  
  
 gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc 643  
 Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu Asp Glu Gly Ile Gly  
 170 175 180  
  
 gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgc ctc caa gcc 691  
 Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala  
 185 190 195  
  
 ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc cac tcc aac gac 739  
 Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser His Ser Asn Asp  
 200 205 210  
  
 ttc ctc gcc caa ctc tgc aac acc gca ctc tgg gtc gac cac gga caa 787  
 Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp Val Asp His Gly Gln  
 215 220 225  
  
 atc cgc gaa gcg gga cta gtt cca gac gtg gtg gaa gcc tac gaa ggc 835  
 Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val Glu Ala Tyr Glu Gly  
 230 235 240 245  
  
 aag ggc gcc ggc gac cac gtc cgc aga ctc ctc acc cgc atg gaa gaa 883  
 Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu Thr Arg Met Glu Glu  
 250 255 260  
  
 gaa aag tagctcctgc gtttcggggtt tgc 912  
 Glu Lys

&lt;210&gt; 144

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 144

Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe  
 1 5 10 15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly  
 20 25 30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu  
 35 40 45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val  
 50 55 60  
 Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly  
 65 70 75 80  
 Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala  
 85 90 95  
 Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr  
 100 105 110  
 Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln  
 115 120 125  
 Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu  
 130 135 140  
 Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg  
 145 150 155 160  
 Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu  
 165 170 175  
 Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg  
 180 185 190  
 Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala  
 195 200 205  
 Ser His Ser Asn Asp Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp  
 210 215 220  
 Val Asp His Gly Gln Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val  
 225 230 235 240  
 Glu Ala Tyr Glu Gly Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu  
 245 250 255  
 Thr Arg Met Glu Glu Glu Lys  
 260

&lt;210&gt; 145

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(775)

&lt;223&gt; FRXA00431

&lt;400&gt; 145

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 tggcgattcc ggcgcagcta ctgggtataa ggagcaccac atg gta tcc atc gat 115  
 Met Val Ser Ile Asp  
 1 5

aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163

Thr	Tyr	Asn	Ala	Cys	Val	Asp	Phe	Pro	Ile	Phe	Asp	Ala	Lys	Ser	Arg	
				10					15					20		
tcc	atg	aag	aaa	gcc	ttc	ctc	ggc	gca	gcc	ggc	gga	gca	atc	ggg	cgc	211
Ser	Met	Lys	Lys	Ala	Phe	Leu	Gly	Ala	Ala	Gly	Gly	Ala	Ile	Gly	Arg	
			25					30					35			
aat	caa	gac	aac	gtc	gta	gtc	gtc	gaa	gcg	ctg	aag	aac	gtc	aac	ctg	259
Asn	Gln	Asp	Asn	Val	Val	Val	Val	Glu	Ala	Leu	Lys	Asn	Val	Asn	Leu	
		40					45					50				
cac	ttg	cgc	gaa	ggg	gac	cgg	gtc	gga	ctc	gtc	ggc	cac	aac	ggc	gcc	307
His	Leu	Arg	Glu	Gly	Asp	Arg	Val	Gly	Leu	Val	Gly	His	Asn	Gly	Ala	
	55					60					65					
ggc	aaa	tcc	acc	ctc	ctg	cga	ctc	ctc	tcc	ggc	atc	tac	gaa	ccc	acc	355
Gly	Lys	Ser	Thr	Leu	Leu	Arg	Leu	Leu	Ser	Gly	Ile	Tyr	Glu	Pro	Thr	
	70				75				80						85	
cgc	gga	agc	gct	gac	atc	cgt	gga	cgc	gtc	gcc	ccc	gtc	ttc	gac	ctc	403
Arg	Gly	Ser	Ala	Asp	Ile	Arg	Gly	Arg	Val	Ala	Pro	Val	Phe	Asp	Leu	
				90					95					100		
ggc	gtc	ggc	atg	gat	cca	gaa	atc	tcc	ggc	tac	gaa	aat	atc	atc	atc	451
Gly	Val	Gly	Met	Asp	Pro	Glu	Ile	Ser	Gly	Tyr	Glu	Asn	Ile	Ile	Ile	
			105					110					115			
cgc	ggc	ctc	ttc	ctc	ggg	caa	acc	cgc	aaa	cag	atg	aaa	gcc	aaa	atg	499
Arg	Gly	Leu	Phe	Leu	Gly	Gln	Thr	Arg	Lys	Gln	Met	Lys	Ala	Lys	Met	
		120					125					130				
gaa	gaa	atc	gcc	gac	ttc	acc	gaa	ctc	ggc	gaa	tac	ctc	tcc	atg	cct	547
Glu	Glu	Ile	Ala	Asp	Phe	Thr	Glu	Leu	Gly	Glu	Tyr	Leu	Ser	Met	Pro	
	135					140					145					
ctc	cga	acc	tac	tcc	acc	ggc	atg	cgc	atc	cgc	cta	gcc	ctc	ggc	gtg	595
Leu	Arg	Thr	Tyr	Ser	Thr	Gly	Met	Arg	Ile	Arg	Leu	Ala	Leu	Gly	Val	
	150				155				160						165	
gtc	acc	tcc	atc	gag	ccc	gaa	att	ctg	ctt	ctt	gat	gaa	ggc	atc	ggc	643
Val	Thr	Ser	Ile	Glu	Pro	Glu	Ile	Leu	Leu	Leu	Asp	Glu	Gly	Ile	Gly	
				170				175						180		
gcc	gtc	gac	gcc	gcc	ttc	atg	gcc	aaa	gcc	cgc	gac	cgg	ctc	caa	gcc	691
Ala	Val	Asp	Ala	Ala	Phe	Met	Ala	Lys	Ala	Arg	Asp	Arg	Leu	Gln	Ala	
			185					190					195			
ctc	gtc	gaa	cga	tcc	ggc	atc	ctc	gtc	ttc	gcc	tcc	act	caa	cga	ctt	739
Leu	Val	Glu	Arg	Ser	Gly	Ile	Leu	Val	Phe	Ala	Ser	Thr	Gln	Arg	Leu	
		200				205						210				
tct	tgc	caa	ctc	tgc	aac	acc	gca	ctc	tgg	gtc	gac					775
Ser	Cys	Gln	Leu	Cys	Asn	Thr	Ala	Leu	Trp	Val	Asp					
	215				220						225					

&lt;210&gt; 146

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

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Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe
 1              5              10              15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly
          20              25              30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu
          35              40              45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
          50              55              60

Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
          65              70              75              80

Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
          85              90              95

Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr
          100              105              110

Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln
          115              120              125

Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu
          130              135              140

Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
          145              150              155              160

Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
          165              170              175

Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
          180              185              190

Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
          195              200              205

Ser Thr Gln Arg Leu Ser Cys Gln Leu Cys Asn Thr Ala Leu Trp Val
          210              215              220

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Asp  
225

&lt;210&gt; 147

&lt;211&gt; 1670

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1647)

&lt;223&gt; RXN00732

&lt;400&gt; 147

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aat cac ctc ctc cta ctc ccc acg gta aag gca gac atc att gac aat      48
Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
 1              5              10              15

```

ggt gtg gtc aca ggt gac atc ggc tat att tgg cac acc ggt gga atc Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile 20 25 30	96
atg ctg gcc ctg aca tta gtc cag gtt gcc tgc gct atc gcc ggt gtt Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val 35 40 45	144
tat ttc ggt tcc aaa cta tcc atg aga gtg ggc cgc gat ctg cgt tcg Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser 50 55 60	192
gcg atc ttt ggc aag gta gtg aac ttc tct gag cgt gag atg ggt cag Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln 65 70 75 80	240
ttt ggc gca ccg tcg ctg atc acc cga aac acc aac gat gtg cag cag Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln 85 90 95	288
gtt cag atg ctg gtg cag atg acc tcc act ttg atg att tcc gcc ccg Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro 100 105 110	336
atg ctg gcc att ggt ggc atc atc atg gcg gtg cgt cag gat ctt ggt Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly 115 120 125	384
ttg tct tgg ctg atg gtg gtc agt att ccg gtg ctc atc atc gtg gtg Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val 130 135 140	432
gcg ctg atc att gtg cgc atg gtt ccg ttg ttc caa acc atg caa aag Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys 145 150 155 160	480
cgc att gac cgc atc aat cag att ata cgc gag cag ctc acc ggt atc Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile 165 170 175	528
cgc gtg atc cgc gcg ttc gtg cgt gaa gat gtg gaa cgc gaa cga ttc Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe 180 185 190	576
acc act gct agt aaa gat gtc gct gat atc ggc gtg cgc acc ggt aac Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn 195 200 205	624
ctg atg gcg ttg atg ttc cct gcc gtg atg ctg atc atg aac ctt tct Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser 210 215 220	672
gcc gtt gct gtg att tgg ttt ggt gct ttc cag gtg gaa tcc ggc gag Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu 225 230 235 240	720
acg cag atc ggt acg ctc ttt gca ttc ttg cag tac atc atg cag atc Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile 245 250 255	768

ctc atg ggc gtc atg atg gca gcg ttc atg ttt gtc atg gtt ccg cgc	816
Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg	
260 265 270	
gct gcc gtt tcc gct gat cgc atc ggt gag gtt ctg gaa acc aca ccg	864
Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro	
275 280 285	
tct gtg cag gcg cca gaa aca ccg gcg cag ccg tcg aca agc gct ggc	912
Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly	
290 295 300	
gaa atc gtg ttc aac aac gcg act ttt gcc tac ccc ggc gcg gat gac	960
Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp	
305 310 315 320	
ccc gtg tta aat aat gtg agc ttc cgc gtt gcg cct ggt agc acg acg	1008
Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr	
325 330 335	
gcg atc atc ggc tcg acg ggt tcg ggt aag acg acg ttg atc ggg ctg	1056
Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu	
340 345 350	
gtt cct agg ctt ttc gac gtc acc gaa ggc gac gtt acc gtc gat ggc	1104
Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly	
355 360 365	
acc gat gtt cgt gaa ttt gag ccg ctg aag ctg tgg gat cgg atc ggt	1152
Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly	
370 375 380	
ctt gtt ccg cag aag tcg ttc ctg ttt tct gga acg atc gcc agc aac	1200
Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn	
385 390 395 400	
ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg cag gcg	1248
Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala	
405 410 415	
ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca gag ggt	1296
Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly	
420 425 430	
ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt ggt cag	1344
Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln	
435 440 445	
cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct gag atc	1392
Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile	
450 455 460	
tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca gac gcc	1440
Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala	
465 470 475 480	
gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc aag ttg	1488
Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu	
485 490 495	
att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag att gtg	1536

Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val  
500 505 510

gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg aat ttg 1584  
Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu  
515 520 525

ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa gag act 1632  
Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr  
530 535 540

gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc 1670  
Ala Gln Ala Gln Ser  
545

&lt;210&gt; 148

&lt;211&gt; 549

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 148

Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn  
1 5 10 15

Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile  
20 25 30

Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val  
35 40 45

Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser  
50 55 60

Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln  
65 70 75 80

Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln  
85 90 95

Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro  
100 105 110

Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly  
115 120 125

Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val  
130 135 140

Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys  
145 150 155 160

Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile  
165 170 175

Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe  
180 185 190

Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn  
195 200 205



Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser  
 210 215 220  
 Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu  
 225 230 235 240  
 Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile  
 245 250 255  
 Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg  
 260 265 270  
 Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro  
 275 280 285  
 Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly  
 290 295 300  
 Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp  
 305 310 315 320  
 Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr  
 325 330 335  
 Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu  
 340 345 350  
 Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly  
 355 360 365  
 Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly  
 370 375 380  
 Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn  
 385 390 395 400  
 Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala  
 405 410 415  
 Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly  
 420 425 430  
 Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln  
 435 440 445  
 Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile  
 450 455 460  
 Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala  
 465 470 475 480  
 Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu  
 485 490 495  
 Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val  
 500 505 510  
 Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu  
 515 520 525  
 Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr

530

535

540

Ala Gln Ala Gln Ser  
545

<210> 149  
<211> 922  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(922)  
<223> FRXA00732

<400> 149  
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ctgatcaccc cgaaacacca acgatgtgca gcaggttcag atg ctg gtg cag atg 115  
Met Leu Val Gln Met  
1 5  
acc tcc act ttg atg att tcc gcc ccg atg ctg gcc att ggt ggc atc 163  
Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu Ala Ile Gly Gly Ile  
10 15 20  
atc atg gcg gtg cgt cag gat ctt ggt ttg tct tgg ctg atg gtg gtc 211  
Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser Trp Leu Met Val Val  
25 30 35  
agt att ccg gtg ctc atc atc gtg gtg gcg ctg atc att gtg cgc atg 259  
Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu Ile Ile Val Arg Met  
40 45 50  
gtt ccg ttg ttc caa acc atg caa aag cgc att gac cgc atc aat cag 307  
Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile Asp Arg Ile Asn Gln  
55 60 65  
att ata cgc gag cag ctc acc ggt atc cgc gtg atc cgc gcg ttc gtg 355  
Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val Ile Arg Ala Phe Val  
70 75 80 85  
cgt gaa gat gtg gaa cgc gaa cga ttc acc act gct agt aaa gat gtc 403  
Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr Ala Ser Lys Asp Val  
90 95 100  
gct gat atc ggc gtg cgc acc ggt aac ctg atg gcg ttg atg ttc cct 451  
Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met Ala Leu Met Phe Pro  
105 110 115  
gcc gtg atg ctg atc atg aac ctt tct gcc gtt gct gtg att tgg ttt 499  
Ala Val Met Leu Ile Met Asn Leu Ser Ala Val Ala Val Ile Trp Phe  
120 125 130  
ggt gct ttc cag gtg gaa tcc ggc gag acg cag atc ggt acg ctc ttt 547  
Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln Ile Gly Thr Leu Phe  
135 140 145  
gca ttc ttg cag tac atc atg cag atc ctc atg ggc gtc atg atg gca 595  
Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met Gly Val Met Met Ala

150	155	160	165	
gcg ttc atg ttt gtc atg gtt ccg cgc gct gcc gtt tcc gct gat cgc				643
Ala Phe Met Phe Val Met Val Pro Arg Ala Ala Val Ser Ala Asp Arg				
	170	175	180	
atc ggt gag gtt ctg gaa acc aca ccg tct gtg cag gcg cca gaa aca				691
Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val Gln Ala Pro Glu Thr				
	185	190	195	
ccg gcg cag ccg tcg aca agc gct ggc gaa atc gtg ttc aac aac gcg				739
Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile Val Phe Asn Asn Ala				
	200	205	210	
act ttt gcc tac ccc ggc gcg gat gac ccc gtg tta aat aat gtg agc				787
Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val Leu Asn Asn Val Ser				
	215	220	225	
ttc cgc gtt gcg cct ggt agc acg acg gcg atc atc ggc tcg acg ggt				835
Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile Ile Gly Ser Thr Gly				
	230	235	240	245
tcg ggt aag acg acg ttg atc ggg ctg gtt cct agg ctt ttc gac gtc				883
Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro Arg Leu Phe Asp Val				
	250	255	260	
acc gaa ggc gac gtt acc gtc gat ggc acc gat gtt cgt				922
Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp Val Arg				
	265	270		

&lt;210&gt; 150

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 150

Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu
1 5 10 15

Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser
20 25 30

Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu
35 40 45

Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile
50 55 60

Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val
65 70 75 80

Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr
85 90 95

Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met
100 105 110

Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser Ala Val
115 120 125

Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln  
 130 135 140

Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met  
 145 150 155 160

Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg Ala Ala  
 165 170 175

Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val  
 180 185 190

Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile  
 195 200 205

Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val  
 210 215 220

Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile  
 225 230 235 240

Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro  
 245 250 255

Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp  
 260 265 270

Val Arg

<210> 151  
 <211> 476  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(453)  
 <223> FRXA00734

<400> 151  
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 Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp  
 1 5 10 15

cag gcg ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca 96  
 Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro  
 20 25 30

gag ggt ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt 144  
 Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly  
 35 40 45

ggt cag cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct 192  
 Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro  
 50 55 60

gag atc tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca 240  
 Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr  
 65 70 75 80

gac gcc gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc 288  
 Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr  
                   85                  90                  95

aag ttg att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag 336  
 Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln  
                   100                  105                  110

att gtg gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg 384  
 Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr  
                   115                  120                  125

aat ttg ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa 432  
 Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln  
                   130                  135                  140

gag act gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc 476  
 Glu Thr Ala Gln Ala Gln Ser  
 145                  150

<210> 152

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp  
   1                  5                  10                  15

Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro  
                   20                  25                  30

Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly  
                   35                  40                  45

Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro  
                   50                  55                  60

Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr  
   65                  70                  75                  80

Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr  
                   85                  90                  95

Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln  
                   100                  105                  110

Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr  
                   115                  120                  125

Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln  
                   130                  135                  140

Glu Thr Ala Gln Ala Gln Ser  
 145                  150

<210> 153

<211> 1172

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1149)

&lt;223&gt; RXN01808

&lt;400&gt; 153

cag agc ctc gcg tgt aaa gaa ctc gca tgg atg cgc ggc ggt gca cca	48
Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro	
1 5 10 15	
gcg cga acc tca aag cct gga ttc cgc ctt gaa gcc gcg gaa gct ttg	96
Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu	
20 25 30	
atc gca gaa gtg cca gcg cca cgc gac aaa gtc gag ctc atg gca ttt	144
Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe	
35 40 45	
tcc aag tcc agg caa ggc cgc gtt gtc att gaa ctt gaa gac gcc aca	192
Ser Lys Ser Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr	
50 55 60	
gta gcc acc cct gat gat cgc atc ctg gta gaa gac ctc acc tgg cgt	240
Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg	
65 70 75 80	
ttg gct cca gga gag cgc atc ggt ctt gtc ggc gtc aac ggc tcc ggc	288
Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly	
85 90 95	
aaa acc acc ctg ctg cgc acc ctt gcc ggc gag cag cca ctt cag gca	336
Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala	
100 105 110	
ggc aaa cgc atc gaa ggc caa acc gtc aaa ctg gga tgg ctc cgc cag	384
Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln	
115 120 125	
gaa ctc gat gac cta gac ctc agc cgc cga ctc atc gac tgc gtt gaa	432
Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu	
130 135 140	
gat gtc gct tcc tac gtg atg atg ggc gac aag cag gtc tcc gct tcc	480
Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser	
145 150 155 160	
caa ttg gca gaa cgc ctc gga ttc tca ccc aag agg caa cgc acc cca	528
Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro	
165 170 175	
gtt ggt gac ctg tcc ggt ggt gaa cgc cgc cga ctc caa ctc acc cgc	576
Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg	
180 185 190	
gtg ctc atg gcc gaa cca aac gtg ctg ctc ctc gac gag ccc acc aac	624
Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn	
195 200 205	

gac ctg gac att gac acc ctc caa gag ctg gaa tcc ctt ctc gac gga 672  
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly  
 210 215 220

tgg cca ggc acc atg gtg gtt atc tcc cac gac cgt tac ctc atc gaa 720  
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu  
 225 230 235 240

cgc gtc acc gac tcc acc tgg gca ctc ttc ggc gat ggc aag ctc acc 768  
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr  
 245 250 255

aac ctg cca ggc gga att gaa gag tac ctg cag cga cga gca gcg atg 816  
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met  
 260 265 270

gcc gcg gcc gaa gac agt gga gtg ctg aac ttg ggt gcg gcc acg cag 864  
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln  
 275 280 285

gct gga acc ttt tct gct gca aca gag cag gct gcc act tct gtg gaa 912  
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu  
 290 295 300

agt tcc gga att tct tcc caa gaa cgc cac cgc atc acc aag gaa atg 960  
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met  
 305 310 315 320

aac gcc ctg gag cgc aaa atg ggc aag ctt gac cag caa atg gac aag 1008  
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys  
 325 330 335

ctt aat cag cag ctc gct gat gca gcg gag gcc atg gac acc ata aag 1056  
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys  
 340 345 350

ctc acc gag ctg gac acc aag ctc cgc gca gtg cag gaa gaa cac ggc 1104  
 Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly  
 355 360 365

gag ctg gaa atg cag tgg ctg gaa ctc ggc gag gaa atc gag ggc 1149  
 Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly  
 370 375 380

tagttcatgc cgtcggcagg cga 1172

&lt;210&gt; 154

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 154

Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro  
 1 5 10 15

Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu  
 20 25 30

Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe  
 35 40 45

Ser Lys Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr  
 50 55 60  
 Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg  
 65 70 75 80  
 Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly  
 85 90 95  
 Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala  
 100 105 110  
 Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln  
 115 120 125  
 Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu  
 130 135 140  
 Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser  
 145 150 155 160  
 Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro  
 165 170 175  
 Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg  
 180 185 190  
 Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn  
 195 200 205  
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly  
 210 215 220  
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu  
 225 230 235 240  
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr  
 245 250 255  
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met  
 260 265 270  
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln  
 275 280 285  
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu  
 290 295 300  
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met  
 305 310 315 320  
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys  
 325 330 335  
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys  
 340 345 350  
 Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly  
 355 360 365



Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly  
 370 375 380

<210> 155  
 <211> 1142  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1119)  
 <223> FRXA01808

<400> 155  
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 Met Arg Gly Gly Ala Pro Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu  
 1 5 10 15  
 gaa gcc gcg gaa gct ttg atc gca gaa gtg cca gcg cca cgc gac aaa 96  
 Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys  
 20 25 30  
 gtc gag ctc atg gca ttt tcc aag tcc agg caa ggc cgc gtt gtc att 144  
 Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile  
 35 40 45  
 gaa ctt gaa gac gcc aca gta gcc acc cct gat gat cgc atc ctg gta 192  
 Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val  
 50 55 60  
 gaa gac ctc acc tgg cgt ttg gct cca gga gag cgc atc ggt ctt gtc 240  
 Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val  
 65 70 75 80  
 ggc gtc aac ggc tcc ggc aaa acc acc ctg ctg cgc acc ctt gcc ggc 288  
 Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly  
 85 90 95  
 gag cag cca ctt cag gca ggc aaa cgc atc gaa ggc caa acc gtc aaa 336  
 Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys  
 100 105 110  
 ctg gga tgg ctc cgc cag gaa ctc gat gac cta gac ctc agc cgc cga 384  
 Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg  
 115 120 125  
 ctc atc gac tgc gtt gaa gat gtc gct tcc tac gtg atg atg ggc gac 432  
 Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp  
 130 135 140  
 aag cag gtc tcc gct tcc caa ttg gca gaa cgc ctc gga ttc tca ccc 480  
 Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro  
 145 150 155 160  
 aag agg caa cgc acc cca gtt ggt gac ctg tcc ggt ggt gaa cgc cgc 528  
 Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg  
 165 170 175  
 cga ctc caa ctc acc cgc gtg ctc atg gcc gaa cca aac gtg ctg ctc 576  
 Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu

180	185	190	
ctc gac gag ccc acc aac gac ctg gac att gac acc ctc caa gag ctg Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu 195 200 205			624
gaa tcc ctt ctc gac gga tgg cca ggc acc atg gtg gtt atc tcc cac Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His 210 215 220			672
gac cgt tac ctc atc gaa cgc gtc acc gac tcc acc tgg gca ctc ttc Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe 225 230 235 240			720
ggc gat ggc aag ctc acc aac ctg cca ggc gga att gaa gag tac ctg Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu 245 250 255			768
cag cga cga gca gcg atg gcc gcg gcc gaa gac agt gga gtg ctg aac Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn 260 265 270			816
ttg ggt gcg gcc acg cag gct gga acc ttt tct gct gca aca gag cag Leu Gly Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln 275 280 285			864
gct gcc act tct gtg gaa agt tcc gga att tct tcc caa gaa cgc cac Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His 290 295 300			912
cgc atc acc aag gaa atg aac gcc ctg gag cgc aaa atg ggc aag ctt Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu 305 310 315 320			960
gac cag caa atg gac aag ctt aat cag cag ctc gct gat gca gcg gag Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu 325 330 335			1008
gcc atg gac acc ata aag ctc acc gag ctg gac acc aag ctc cgc gca Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala 340 345 350			1056
gtg cag gaa gaa cac ggc gag ctg gaa atg cag tgg ctg gaa ctc ggc Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly 355 360 365			1104
gag gaa atc gag ggc tagttcatgc cgtcggcagg cga Glu Glu Ile Glu Gly 370			1142

&lt;210&gt; 156

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

Met	Arg	Gly	Gly	Ala	Pro	Ala	Arg	Thr	Ser	Lys	Pro	Gly	Phe	Arg	Leu
1				5					10					15	

Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys

20										25					30				
Val	Glu	Leu	Met	Ala	Phe	Ser	Lys	Ser	Arg	Gln	Gly	Arg	Val	Val	Ile				
		35					40					45							
Glu	Leu	Glu	Asp	Ala	Thr	Val	Ala	Thr	Pro	Asp	Asp	Arg	Ile	Leu	Val				
	50					55					60								
Glu	Asp	Leu	Thr	Trp	Arg	Leu	Ala	Pro	Gly	Glu	Arg	Ile	Gly	Leu	Val				
65					70					75					80				
Gly	Val	Asn	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Leu	Arg	Thr	Leu	Ala	Gly				
				85					90					95					
Glu	Gln	Pro	Leu	Gln	Ala	Gly	Lys	Arg	Ile	Glu	Gly	Gln	Thr	Val	Lys				
		100						105					110						
Leu	Gly	Trp	Leu	Arg	Gln	Glu	Leu	Asp	Asp	Leu	Asp	Leu	Ser	Arg	Arg				
		115					120					125							
Leu	Ile	Asp	Cys	Val	Glu	Asp	Val	Ala	Ser	Tyr	Val	Met	Met	Gly	Asp				
130						135					140								
Lys	Gln	Val	Ser	Ala	Ser	Gln	Leu	Ala	Glu	Arg	Leu	Gly	Phe	Ser	Pro				
145					150					155					160				
Lys	Arg	Gln	Arg	Thr	Pro	Val	Gly	Asp	Leu	Ser	Gly	Gly	Glu	Arg	Arg				
				165					170					175					
Arg	Leu	Gln	Leu	Thr	Arg	Val	Leu	Met	Ala	Glu	Pro	Asn	Val	Leu	Leu				
			180					185					190						
Leu	Asp	Glu	Pro	Thr	Asn	Asp	Leu	Asp	Ile	Asp	Thr	Leu	Gln	Glu	Leu				
	195						200					205							
Glu	Ser	Leu	Leu	Asp	Gly	Trp	Pro	Gly	Thr	Met	Val	Val	Ile	Ser	His				
210						215					220								
Asp	Arg	Tyr	Leu	Ile	Glu	Arg	Val	Thr	Asp	Ser	Thr	Trp	Ala	Leu	Phe				
225					230				235					240					
Gly	Asp	Gly	Lys	Leu	Thr	Asn	Leu	Pro	Gly	Gly	Ile	Glu	Glu	Tyr	Leu				
			245						250					255					
Gln	Arg	Arg	Ala	Ala	Met	Ala	Ala	Ala	Glu	Asp	Ser	Gly	Val	Leu	Asn				
			260					265					270						
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Gly	Thr	Phe	Ser	Ala	Ala	Thr	Glu	Gln				
	275						280					285							
Ala	Ala	Thr	Ser	Val	Glu	Ser	Ser	Gly	Ile	Ser	Ser	Gln	Glu	Arg	His				
290						295					300								
Arg	Ile	Thr	Lys	Glu	Met	Asn	Ala	Leu	Glu	Arg	Lys	Met	Gly	Lys	Leu				
305					310					315					320				
Asp	Gln	Gln	Met	Asp	Lys	Leu	Asn	Gln	Gln	Leu	Ala	Asp	Ala	Ala	Glu				
			325						330					335					
Ala	Met	Asp	Thr	Ile	Lys	Leu	Thr	Glu	Leu	Asp	Thr	Lys	Leu	Arg	Ala				
			340					345					350						

Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly  
 355 360 365

Glu Glu Ile Glu Gly  
 370

<210> 157  
 <211> 349  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(349)  
 <223> RXN02975

<400> 157  
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 tttattgacc tggcaacttc aattgataga ctgttaggtt gtg att gtc acc aat 115  
 Val Ile Val Thr Asn  
 1 5  
 gat tta gag gtg cgc gtt ggc gca cgt acc ctt ctc gat gcc cca ggt 163  
 Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu Leu Asp Ala Pro Gly  
 10 15 20  
 cag ctc ctt cgg gtg cag cca ggc gac cgt att ggt ctg gtt ggt aga 211  
 Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile Gly Leu Val Gly Arg  
 25 30 35  
 aat ggt gcg ggc aaa acc acc acc atg cga atc ctc tcg ggc gaa acc 259  
 Asn Gly Ala Gly Lys Thr Thr Thr Met Arg Ile Leu Ser Gly Glu Thr  
 40 45 50  
 aag ccc tac gga gga tcc gta acc aca tct ggt gaa atc ggt tac ctg 307  
 Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly Glu Ile Gly Tyr Leu  
 55 60 65  
 ccc cag gac tcc cgc gaa ggc aac atc gaa caa acc gcc cgc 349  
 Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln Thr Ala Arg  
 70 75 80

<210> 158  
 <211> 83  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 158  
 Val Ile Val Thr Asn Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu  
 1 5 10 15  
 Leu Asp Ala Pro Gly Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile  
 20 25 30  
 Gly Leu Val Gly Arg Asn Gly Ala Gly Lys Thr Thr Thr Met Arg Ile  
 35 40 45

Leu Ser Gly Glu Thr Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly  
50 55 60

Glu Ile Gly Tyr Leu Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln  
65 70 75 80

Thr Ala Arg

<210> 159

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN03116

<400> 159

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ttttgctcag gtactgtcac tggaaatcggg aaggctgaaa atg ggg gag ggg gac 115  
Met Gly Glu Gly Asp  
1 5

gtc gaa aag cat ttt gct ttt ggt ctt aaa gct gcg aag cag cgt cgc 163  
Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala Ala Lys Gln Arg Arg  
10 15 20

ttt ttc gcg cgt acc gtg gcc ctc atg cca cag aat cct act att cct 211  
Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln Asn Pro Thr Ile Pro  
25 30 35

gca ggt ctg agc gtt ttt gat tat gtg ctg ctg ggg cgt cat ccg cac 259  
Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu Gly Arg His Pro His  
40 45 50

agt tac gcg ccg ggg cgt gct gat gat gag atc gtg aag ccg tgc ctc 307  
Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile Val Lys Arg Cys Leu  
55 60 65

gct gat ctg aaa ttg gag cat ttc agc gac cgc ggc tta gac gaa ttg 355  
Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg Gly Leu Asp Glu Leu  
70 75 80 85

tcc ggc ggc gag cgt caa cgc gtc agc ctt gcc cgc gcg ctc gcc caa 403  
Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala Arg Ala Leu Ala Gln  
90 95 100

gaa ccg cgc atc gtg ctt ctc gac gag ccg acc tcc gcg ctt gac atc 451  
Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Ile  
105 110 115

ggc cat gcg cag gaa acg ctt gag ctt atc gac gcc atc ccg cac cga 499  
Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp Ala Ile Arg His Arg  
120 125 130

ctc ggc ctc acc gtg atc gcg gcg atg cat gac ctc acc ctg act gcg 547  
Leu Gly Leu Thr Val Ile Ala Ala Met His Asp Leu Thr Leu Thr Ala

135                                      140                                      145

caa tac ggc gat cgg gtg ctc atg atg aat ggt ggc cgc aaa gtt ttc      595  
 Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly Gly Arg Lys Val Phe  
 150                                      155                                      160                                      165

gag ggc act gca gcc gaa gtg ctc acc gcg cag cgg att tcg gag att      643  
 Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln Arg Ile Ser Glu Ile  
    170                                      175                                      180

tat gat gcc act gtg att gtt gag gtt att gat ggg cgt ccc gtg gtg      691  
 Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp Gly Arg Pro Val Val  
    185                                      190                                      195

att ccg caa cgg tcg cac tgacctgttg tggcagacca gac      732  
 Ile Pro Gln Arg Ser His  
    200

&lt;210&gt; 160

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 160

Met Gly Glu Gly Asp Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala  
 1                                      5                                      10                                      15

Ala Lys Gln Arg Arg Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln  
    20                                      25                                      30

Asn Pro Thr Ile Pro Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu  
    35                                      40                                      45

Gly Arg His Pro His Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile  
    50                                      55                                      60

Val Lys Arg Cys Leu Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg  
 65                                      70                                      75                                      80

Gly Leu Asp Glu Leu Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala  
    85                                      90                                      95

Arg Ala Leu Ala Gln Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr  
    100                                      105                                      110

Ser Ala Leu Asp Ile Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp  
    115                                      120                                      125

Ala Ile Arg His Arg Leu Gly Leu Thr Val Ile Ala Ala Met His Asp  
 130                                      135                                      140

Leu Thr Leu Thr Ala Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly  
 145                                      150                                      155                                      160

Gly Arg Lys Val Phe Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln  
    165                                      170                                      175

Arg Ile Ser Glu Ile Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp  
    180                                      185                                      190

Gly Arg Pro Val Val Ile Pro Gln Arg Ser His  
195 200

<210> 161  
<211> 390  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(367)  
<223> RXN03108

<400> 161  
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cttgaccacc tcatcggtga gttgcagaaa gtagtctgct atg act aaa cca aac 115  
Met Thr Lys Pro Asn  
1 5  
gct tcc gtc gag ctg aat acg atc acc aag tcc tac ggc tcc acc act 163  
Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser Tyr Gly Ser Thr Thr  
10 15 20  
atc att ggc gat acg agc atc acc atc aac gac ggt gaa ttc gtc tcc 211  
Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp Gly Glu Phe Val Ser  
25 30 35  
ctc ctc gac cct tcc ggc tgc gga aaa tca aca att ctc aaa atg atc 259  
Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr Ile Leu Lys Met Ile  
40 45 50  
gcc gga ctg gcc tcc cca tcc acc ggc aca gtc agc gca ggc aac gaa 307  
Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val Ser Ala Gly Asn Glu  
55 60 65  
gaa att aaa gga cca gga cct gac cga ggc atg gtt ttc caa gac cac 355  
Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met Val Phe Gln Asp His  
70 75 80 85  
gcc ctc ctg ccc tgattgaccg cacgcggcaa cat 390  
Ala Leu Leu Pro

<210> 162  
<211> 89  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 162  
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20 25 30  
Gly Glu Phe Val Ser Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr  
35 40 45

Ile Leu Lys Met Ile Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val  
50 55 60

Ser Ala Gly Asn Glu Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met  
65 70 75 80

Val Phe Gln Asp His Ala Leu Leu Pro  
85

<210> 163

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN03129

<400> 163

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tccgagcact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc 115  
Met Ala Ser Ile Val  
1 5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc 163  
Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val  
10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211  
Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val  
25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259  
Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly  
40 45 50

ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc 307  
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala  
55 60 65

acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc 355  
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser  
70 75 80 85

tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg 403  
Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala  
90 95 100

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct 451  
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala  
105 110 115

gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct 499  
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro  
120 125 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca 547  
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala



135	140	145	
att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn 150 155 160 165			595
cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu 170 175 180			643
cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val 185 190 195			691
gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val 200 205 210			739
ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn 215 220 225			787
gcg ttc gtc gcc agc ttc att ggt tcc cct tcc atg aac ttg att gag Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser Met Asn Leu Ile Glu 230 235 240 245			835
ggc acc atc cgt ggc gat aag gtc act ttg ggt act gga att cag att Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly Thr Gly Ile Gln Ile 250 255 260			883
tca gtt cct gat gag gtg gca gca gag gtt cgc aac aac ccg gat cgc Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg Asn Asn Pro Asp Arg 265 270 275			931
ttt gag ggt cgt cca gtc att gtt ggt gct cgt ccc gag cac atg tat Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg Pro Glu His Met Tyr 280 285 290			979
ttg acc acg gcg aat gag agt ggt gct gta ttg ggc gaa gtc agc cac Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu Gly Glu Val Ser His 295 300 305			1027
att gat gag ctc ggc gcg gat tca atg gtc tac gta ttg gcg tct ggt Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr Val Leu Ala Ser Gly 310 315 320 325			1075
gtg aag aac ccg aat act gat ctt ttg ggt gag ggc att cca gag gat Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu Gly Ile Pro Glu Asp 330 335 340			1123
atg cgc gtg acc gtt gtc ggt gct gaa gag acc gat aag gcc cgc ctg Met Arg Val Thr Val Val Gly Ala Glu Glu Thr Asp Lys Ala Arg Leu 345 350 355			1171
ggt att cgt gtt gag cgc cat cac ggt ctg aag gcc ggc gat aag gtg Gly Ile Arg Val Glu Arg His His Gly Leu Lys Ala Gly Asp Lys Val 360 365 370			1219
cac gtt gtt gct gca ccg aag gat gtt cac ctc ttc gac ggt ctt gat His Val Val Ala Ala Pro Lys Asp Val His Leu Phe Asp Gly Leu Asp 375 380 385			1267

ggc cgt cga atc ggt gca tcg gtt cta gct cca gcc cat aca gtc cag 1315  
 Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro Ala His Thr Val Gln  
 390 395 400 405

tct ggt cac tagattatct accagtgcac ctc 1347  
 Ser Gly His

<210> 164

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly  
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 Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu  
 35 40 45  
 Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile  
 50 55 60  
 Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala  
 65 70 75 80  
 Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp  
 85 90 95  
 Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile  
 100 105 110  
 Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr  
 115 120 125  
 Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val  
 130 135 140  
 Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp  
 145 150 155 160  
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala  
 165 170 175  
 Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val  
 180 185 190  
 Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val  
 195 200 205  
 Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr  
 210 215 220  
 Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser  
 225 230 235 240

Met Asn Leu Ile Glu Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly  
 245 250 255

Thr Gly Ile Gln Ile Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg  
 260 265 270

Asn Asn Pro Asp Arg Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg  
 275 280 285

Pro Glu His Met Tyr Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu  
 290 295 300

Gly Glu Val Ser His Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr  
 305 310 315 320

Val Leu Ala Ser Gly Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu  
 325 330 335

Gly Ile Pro Glu Asp Met Arg Val Thr Val Val Gly Ala Glu Glu Thr  
 340 345 350

Asp Lys Ala Arg Leu Gly Ile Arg Val Glu Arg His His Gly Leu Lys  
 355 360 365

Ala Gly Asp Lys Val His Val Val Ala Ala Pro Lys Asp Val His Leu  
 370 375 380

Phe Asp Gly Leu Asp Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro  
 385 390 395 400

Ala His Thr Val Gln Ser Gly His  
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<210> 165  
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<220>  
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 <223> FRXA01890

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tccgagcact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc 115  
 Met Ala Ser Ile Val  
 1 5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc 163  
 Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val  
 10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211  
 Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val  
 25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259  
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly

40	45	50	
ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc			307
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala			
55	60	65	
acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc			355
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser			
70	75	80	85
tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg			403
Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala			
	90	95	100
ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct			451
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala			
	105	110	115
gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct			499
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro			
	120	125	130
gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca			547
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala			
	135	140	145
att gtg cgt gag cca tgc gtg ttc tgc atg gat gag cca ctg tcc aac			595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn			
150	155	160	165
cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg			643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu			
	170	175	180
cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc			691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val			
	185	190	195
gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg			739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Gly Val			
	200	205	210
ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat			787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn			
	215	220	225
gcg ttc gtc gcc agc ttc att ggt tcc ctt cca tgaacttgat tgagggcacc			840
Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro			
230	235	240	
atc			843

&lt;210&gt; 166

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 166

Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly

1

5

10

15

Ala Arg Pro Ala Val Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu  
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu  
 35 40 45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile  
 50 55 60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala  
 65 70 75 80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp  
 85 90 95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile  
 100 105 110

Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr  
 115 120 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val  
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp  
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala  
 165 170 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val  
 180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val  
 195 200 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr  
 210 215 220

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro  
 225 230 235 240

&lt;210&gt; 167

&lt;211&gt; 1056

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1033)

&lt;223&gt; RXN02945

&lt;400&gt; 167

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tggtgcactt gatcgtttcg cgcctggccg cgaggtataa atg acc acc gca ctt 115

Met Thr Thr Ala Leu

1

5

gga acg cgc gtt gtt gcg cgc aac ttt ggc tac cgc cat gct tcc cgg 163  
 Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr Arg His Ala Ser Arg  
 10 15 20

gaa aac ccc gcg ctc aaa gac atc aac ttc gag atc gca cct ggt gaa 211  
 Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu Ile Ala Pro Gly Glu  
 25 30 35

cgc atc ctg ctc acc ggc gct tcc ggc gcc gga aaa tcc acg cta ctc 259  
 Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Leu  
 40 45 50

gcc gcg ctc gct ggc gtt tta ggc ggt tct gat gag ggc gtt tct acg 307  
 Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp Glu Gly Val Ser Thr  
 55 60 65

ggc gaa ttg ctt gtc gac gcc ccc tcc atc ggt ttg gtt ctc caa gat 355  
 Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly Leu Val Leu Gln Asp  
 70 75 80 85

cca gat tcc caa gtc atc gcc tcc cgc atc ggc gat gat gtg gcg ttt 403  
 Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly Asp Asp Val Ala Phe  
 90 95 100

ggc tgc gaa aac ctc caa att ccg cgc gag gaa atc tgg cca cgg gtg 451  
 Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu Ile Trp Pro Arg Val  
 105 110 115

gaa cga gca ctt gaa ttg gtg ggc ttg gat cta cca ctg agc cac ccc 499  
 Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu Pro Leu Ser His Pro  
 120 125 130

acg aaa tat ctt tcc ggt ggc caa aaa caa cgc ctc gct ctt gcc ggt 547  
 Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg Leu Ala Leu Ala Gly  
 135 140 145

gtg atc gcc atg ggt gct cgt ctg att ctg ctt gat gaa ccc acc gca 595  
 Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu Asp Glu Pro Thr Ala  
 150 155 160 165

aac ctt gat cct caa ggc caa aaa aat gtg gtc gca gca gtg gat cgc 643  
 Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val Ala Ala Val Asp Arg  
 170 175 180

gtt gtt cag gaa act gga gca aca ctc atc gtg gtg gaa cac cgc cat 691  
 Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val Val Glu His Arg His  
 185 190 195

gag ctg tgg gtc aac atc att gac cgg atc atc agt att act gac ggc 739  
 Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile Ser Ile Thr Asp Gly  
 200 205 210

gaa gat gtc caa cct gca gag ttg atc aag gtg ggc cag ttg cct ggg 787  
 Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val Gly Gln Leu Pro Gly  
 215 220 225

gcg cag ccg tcg aca agc aaa ccg atc ttg tgg gcg aat gat ttg ctg 835  
 Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp Ala Asn Asp Leu Leu  
 230 235 240 245

tgc acc tgg ggc ggc ctg cgt agt ttt gag gtg ccg gaa ggc gcc tcg 883

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<211> 311  
<212> PRT  
<213> Corynebacterium glutamicum

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Arg	His	Ala	Ser	Arg	Glu	Asn	Pro	Ala	Leu	Lys	Asp	Ile	Asn	Phe	Glu				
			20					25					30						
Ile	Ala	Pro	Gly	Glu	Arg	Ile	Leu	Leu	Thr	Gly	Ala	Ser	Gly	Ala	Gly				
		35					40					45							
Lys	Ser	Thr	Leu	Leu	Ala	Ala	Leu	Ala	Gly	Val	Leu	Gly	Gly	Ser	Asp				
	50					55					60								
Glu	Gly	Val	Ser	Thr	Gly	Glu	Leu	Leu	Val	Asp	Ala	Pro	Ser	Ile	Gly				
65					70					75					80				
Leu	Val	Leu	Gln	Asp	Pro	Asp	Ser	Gln	Val	Ile	Ala	Ser	Arg	Ile	Gly				
				85					90					95					
Asp	Asp	Val	Ala	Phe	Gly	Cys	Glu	Asn	Leu	Gln	Ile	Pro	Arg	Glu	Glu				
			100					105					110						
Ile	Trp	Pro	Arg	Val	Glu	Arg	Ala	Leu	Glu	Leu	Val	Gly	Leu	Asp	Leu				
		115					120					125							
Pro	Leu	Ser	His	Pro	Thr	Lys	Tyr	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg				
	130					135					140								
Leu	Ala	Leu	Ala	Gly	Val	Ile	Ala	Met	Gly	Ala	Arg	Leu	Ile	Leu	Leu				
145					150					155					160				
Asp	Glu	Pro	Thr	Ala	Asn	Leu	Asp	Pro	Gln	Gly	Gln	Lys	Asn	Val	Val				
				165					170					175					
Ala	Ala	Val	Asp	Arg	Val	Val	Gln	Glu	Thr	Gly	Ala	Thr	Leu	Ile	Val				
			180					185						190					

Val Glu His Arg His Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile  
 195 200 205

Ser Ile Thr Asp Gly Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val  
 210 215 220

Gly Gln Leu Pro Gly Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp  
 225 230 235 240

Ala Asn Asp Leu Leu Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val  
 245 250 255

Pro Glu Gly Ala Ser Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys  
 260 265 270

Ser Thr Leu Ala Leu Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly  
 275 280 285

Ser Trp Asn Ser Leu Thr Arg Cys Ala Ala Ala Leu Thr Arg Pro Arg  
 290 295 300

Thr Ser Gly Val Gln Leu Ile  
 305 310

<210> 169  
 <211> 357  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(334)  
 <223> RXA01247

<400> 169  
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cgcgcctct acaccgtccg cgaccgtctc cgctcggcc gtg gcc gcg gca acc 115  
 Val Ala Ala Ala Thr  
 1 5

gac gca aca cct gaa ggt ccc acc acc tac cag gtc aca ggc atg acc 163  
 Asp Ala Thr Pro Glu Gly Pro Thr Thr Tyr Gln Val Thr Gly Met Thr  
 10 15 20

tgc gga cac tgc gcc gac aac gtc acc gag gcg gtg agc gct ctg ccc 211  
 Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala Val Ser Ala Leu Pro  
 25 30 35

cag gtc gac gac gtc cag gtc gac ctc atc gcc ggt ggg gtc tcc atc 259  
 Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala Gly Gly Val Ser Ile  
 40 45 50

gtc acg gtc acg ggt tcc gtg ccc ctg gaa acc gtc cac cgg gca att 307  
 Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr Val His Arg Ala Ile  
 55 60 65

gag gag acc ggc tac acc gtc ttg tcc tgatcgattc acccatcatc 354  
 Glu Glu Thr Gly Tyr Thr Val Leu Ser



75

tcg

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Val Thr Gly Met Thr Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala
      20                               25                      30
Val Ser Ala Leu Pro Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala
      35                               40                      45
Gly Gly Val Ser Ile Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr
  50                               55                      60
Val His Arg Ala Ile Glu Glu Thr Gly Tyr Thr Val Leu Ser
  65                               70                      75

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<223> RXN00099
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ccgcgcaa																115
aat	aggtagtcgc	ttgcttatag	ggtcaggggc	gtg	aag	aat	cct	cgc								115
Val	Lys	Asn	Pro	Arg								5				
1																
ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca																163
Leu	Ile	Ala	Leu	Ala	Ala	Ile	Ile	Leu	Thr	Ser	Phe	Asn	Leu	Arg	Thr	20
10																
15																
gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta																211
Ala	Ile	Thr	Ala	Leu	Ala	Pro	Leu	Val	Ser	Glu	Ile	Arg	Asp	Asp	Leu	35
25																
30																
ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct																259
Gly	Val	Ser	Ala	Ser	Leu	Ile	Gly	Val	Leu	Gly	Met	Ile	Pro	Thr	Ala	50
40																
45																
50																
atg ttc gcg gat gct gcg ttt gcg ctt ccg tcg ttg aag agg aag ttc																307
Met	Phe	Ala	Asp	Ala	Ala	Phe	Ala	Leu	Pro	Ser	Leu	Lys	Arg	Lys	Phe	65
55																
60																
act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt																355

Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu Leu Thr Ala Ala Gly	
70 75 80 85	
cag att att cgt gtc gct gga cct gct tcg ctg ttg atg gtc ggt act	403
Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr	
90 95 100	
gtg ttc gcg atg ttt gcg atc gga gtt acc aat gtg ttg ctt ccg att	451
Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile	
105 110 115	
gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act	499
Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr	
120 125 130	
tat ctg gtg tcg ttc cag att gtt cag gca ctt gct ccg acg ctt gcc	547
Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu Ala Pro Thr Leu Ala	
135 140 145	
gtg ccg att tct cag tgg gct aca cat gtg ggg ttg acc ggt tgg agg	595
Val Pro Ile Ser Gln Trp Ala Thr His Val Gly Leu Thr Gly Trp Arg	
150 155 160 165	
gtg tcg ctc ggt tcg tgg gcg ctg ctg ggg ttg gtt gcg gcg att tcg	643
Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu Val Ala Ala Ile Ser	
170 175 180	
tgg att ccg ctg ttg agt ttg cag ggt gcc agg gtt gtt gcg gcg ccg	691
Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro	
185 190 195	
tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc	739
Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu	
200 205 210	
ggg ttg atg ttt ggg ttt act tcg ttt gcg acg tat atc ctc atg ggt	787
Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly	
215 220 225	
ttt atg ccg cag atg gta ggt gat cct cag ctc ggt gcg gtg ttg tta	835
Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu	
230 235 240 245	
ggc tgg tgg tca att ttg gga ttg ccg ctg aac att ctg gga ccg tgg	883
Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp	
250 255 260	
ttg gtg acg cgt ttc act aac tgc ttc ccg atg gtt gtt atc gcc agt	931
Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser	
265 270 275	
gtc atg ttt ctc atc ggt aat ggt ggg ttt tgt ttg gct ccg gat gtt	979
Val Met Phe Leu Ile Gly Asn Gly Phe Cys Leu Ala Pro Asp Val	
280 285 290	
gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc	1027
Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu Gly Pro Leu Ala Phe	
295 300 305	
ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt	1075
Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly	

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<210> 172
<211> 391
<212> PRT
<213> Corynebacterium glutamicum
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<400> 172
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20 25 30

Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly  
35 40 45

Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser  
50 55 60

Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu  
65 70 75 80

Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu  
85 90 95

Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn  
100 105 110

Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly  
115 120 125

Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu  
130 135 140

Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly  
145 150 155 160

Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu  
165 170 175

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg  
 180 185 190  
 Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser  
 195 200 205  
 Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr  
 210 215 220  
 Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu  
 225 230 235 240  
 Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn  
 245 250 255  
 Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met  
 260 265 270  
 Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys  
 275 280 285  
 Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu  
 290 295 300  
 Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala  
 305 310 315 320  
 Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu  
 325 330 335  
 Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val  
 340 345 350  
 Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala  
 355 360 365  
 Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr  
 370 375 380  
 Val Glu Lys Leu Leu Asn Arg  
 385 390

<210> 173  
 <211> 1296  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1273)  
 <223> FRXA00099

<400> 173  
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 ccgcgcaaat aggtagtcgc ttgcttatag ggtcaggggc gtg aag aat cct cgc 115  
 Val Lys Asn Pro Arg  
 1 5

ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca 163  
 Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr  
                   10                  15                  20

gct att act gct tta gct ccg ctg gtt tct gag att ccg gat gat tta 211  
 Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu  
                   25                  30                  35

ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct 259  
 Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala  
                   40                  45                  50

atg ttc gcg gat gct gcg ttt gcg ctt ccg tcg ttg aag agg aag ttc 307  
 Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser Leu Lys Arg Lys Phe  
                   55                  60                  65

act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt 355  
 Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu Leu Thr Ala Ala Gly  
                   70                  75                  80                  85

cag att att cgt gtc gct gga cct gct tcg ctg ttg atg gtc ggt act 403  
 Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr  
                   90                  95                  100

gtg ttc gcg atg ttt gcg atc gga gtt acc aat gtg ttg ctt ccg att 451  
 Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile  
                   105                  110                  115

gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act 499  
 Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr  
                   120                  125                  130

tat ctg gtg tcg ttc cag att gtt cag gca ctt gct ccg acg ctt gcc 547  
 Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu Ala Pro Thr Leu Ala  
                   135                  140                  145

gtg ccg att tct cag tgg gct aca cat gtg ggg ttg acc ggt tgg agg 595  
 Val Pro Ile Ser Gln Trp Ala Thr His Val Gly Leu Thr Gly Trp Arg  
                   150                  155                  160                  165

gtg tcg ctc ggt tcg tgg gcg ctg ctg ggg ttg gtt gcg gcg att tcg 643  
 Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu Val Ala Ala Ile Ser  
                   170                  175                  180

tgg att ccg ctg ttg agt ttg cag ggt gcc agg gtt gtt gcg gcg ccg 691  
 Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro  
                   185                  190                  195

tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc 739  
 Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu  
                   200                  205                  210

ggg ttg atg ttt ggg ttt act tcg ttt gcg acg tat atc ctc atg ggt 787  
 Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly  
                   215                  220                  225

ttt atg ccg cag atg gta ggt gat cct cag ctc ggt gcg gtg ttg tta 835  
 Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu  
                   230                  235                  240                  245

ggc tgg tgg tca att ttg gga ttg ccg ctg aac att ctg gga ccg tgg 883

Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp  
 250 255 260

ttg gtg acg cgt ttc act aac tgc ttc ccg atg gtt gtt atc gcc agt 931  
 Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser  
 265 270 275

gtc atg ttt ctc atc ggt aat ggt ggg ttt tgt ttg gct ccg gat gtt 979  
 Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val  
 280 285 290

gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc 1027  
 Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu Gly Pro Leu Ala Phe  
 295 300 305

ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt 1075  
 Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly  
 310 315 320 325

gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg 1123  
 Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala  
 330 335 340

tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gca aca ggc agc 1171  
 Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser  
 345 350 355

ttc cga aca atc ttt ttg ctt ttt gcg ggt gca aca ctc ttc gtt att 1219  
 Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala Thr Leu Phe Val Ile  
 360 365 370

aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta 1267  
 Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu  
 375 380 385

aat cgc taggatggcg ctatgccgca aag 1296  
 Asn Arg  
 390

&lt;210&gt; 174

&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 174

Val Lys Asn Pro Arg Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser  
 1 5 10 15

Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu  
 20 25 30

Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly  
 35 40 45

Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser  
 50 55 60

Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu  
 65 70 75 80



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<220>
<221> CDS
<222> (101)..(1483)
<223> RXA00634
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ggttagggttc aaaagcgcaa cctcaataat cagtattgaa atg tgg gag cga ttc																	115
Met Trp Glu Arg Phe																	
1 5																	
agc ttc tac ggc atg caa gca ctc ttg gtg tac tac ctg tat ttt gat																	163
Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr Tyr Leu Tyr Phe Asp																	
10 15 20																	
ggt gca gcc ggt gga tta ggc ctt gat caa acc caa gca aca gga ctg																	211
Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr Gln Ala Thr Gly Leu																	
25 30 35																	
gtc ggc gtt tat ggc gca ctg ctc tac ctc tgc tgt tgg gca ggc ggt																	259
Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys Cys Trp Ala Gly Gly																	
40 45 50																	
tgg gtc agt gac aga gtc ctg ggc gca gaa aaa acc ctg ctg ggc ggt																	307
Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys Thr Leu Leu Gly Gly																	
55 60 65																	
gcg atc tca gta acc atc gga cac ctt gtg ctt gct ggc ctc ggc ggg																	355
Ala Ile Ser Val Thr Ile Gly His Leu Val Leu Ala Gly Leu Gly Gly																	
70 75 80 85																	
aaa att ggt cta gcc att ggc ctt gga tgc atc gcg atc ggt tca gga																	403
Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile Ala Ile Gly Ser Gly																	
90 95 100																	
ttt gtg aaa aca gca gcc atc acc gtg ctg gga tcc agg cat ggt gaa																	451
Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly Ser Arg His Gly Glu																	
105 110 115																	
caa gaa gga gac gca aag gca gat ccc gca ttc caa ctc ttc tac cta																	499
Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe Gln Leu Phe Tyr Leu																	
120 125 130																	
ggc atc aac gtt ggt gca ctg ctc gga cca ctc ctg acc ggt tgg ctc																	547
Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu Leu Thr Gly Trp Leu																	
135 140 145																	
tcc agc agg tat tcc ttt gaa atg gga ttc ggc gca gcc gca gtc ctt																	595
Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly Ala Ala Ala Val Leu																	
150 155 160 165																	
atg atc ggc gga ttg gga atc tac gca gcg ttg cgg aaa cca atg ctg																	643
Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu Arg Lys Pro Met Leu																	
170 175 180																	



caa tcg ttc ccg ctc gag gtg aag aaa gcg ctg ctc cgc gcc caa aac Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu Leu Arg Ala Gln Asn 185 190 195	691
cct gca gaa aaa cat gtg att agc acg gca ttt gct gca gtg gct gtg Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe Ala Ala Val Ala Val 200 205 210	739
ctt tgc gga gtg ctg ctt tat ctt ctc ctt aca gaa aca gtc agc gca Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr Glu Thr Val Ser Ala 215 220 225	787
gac caa cta gct gga gct ctg ctt tta gta aca atc ggt gca gca cta Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr Ile Gly Ala Ala Leu 230 235 240 245	835
tgg ctc att atc cag ccc tta cga cac cca caa gtc agc tcc gaa gag Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln Val Ser Ser Glu Glu 250 255 260	883
aaa cga aaa gtg ctg gca ttc atc ccg atc ttc gtc tgc tca acc gca Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe Val Cys Ser Thr Ala 265 270 275	931
ttc tgg gca gtg caa gca caa acc tac ggc gta cta gct gtg tac tcc Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val Leu Ala Val Tyr Ser 280 285 290	979
caa gaa cgt gtt gac cgc atg gtt ggc gat ttt gag atc cca gca gcc Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe Glu Ile Pro Ala Ala 295 300 305	1027
tgg tca caa tca ctc aat cct ttt ttc atc ctg gcg ctg tcc atc ccg Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu Ala Leu Ser Ile Pro 310 315 320 325	1075
att tcc ctg tgg ttt atg cgc gga tca cgc gcc cca aga gtg aaa att Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala Pro Arg Val Lys Ile 330 335 340	1123
gga atc agc att gga gtg atc att gcg gga agt ggg ctt cta gtt ctt Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser Gly Leu Leu Val Leu 345 350 355	1171
att cca ttt gtt gga atg ccg ctc gcg cca gtg tgg gtg ctg cct tta Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val Trp Val Leu Pro Leu 360 365 370	1219
agt gtt ttc ctc atc tca ctg gga gaa ctt ttc atc gga ccc gga gga Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe Ile Gly Pro Gly Gly 375 380 385	1267
atg gct gcg act gcg cac cac gca cca cga ata ttt gcc aca cga ttc Met Ala Ala Thr Ala His His Ala Pro Arg Ile Phe Ala Thr Arg Phe 390 395 400 405	1315
tcc gcc ctg tat ttc ctc aca ctc gcc atc ggc atg tct att gca ggt Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly Met Ser Ile Ala Gly 410 415 420	1363
aat gtg tcc aaa ttt tac gac ccc acc aac cac acc tcc gag ctc cga	1411

Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His Thr Ser Glu Leu Arg  
 425 430 435  
 tac ttc gcg gta ttt ggc att tcg atc atc gtc atc ggt gtc ggt tca 1459  
 Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val Ile Gly Val Gly Ser  
 440 445 450  
 ctg atg gtg gcc aag aag gtt gga taacaggggtt aatcttgggt gat 1506  
 Leu Met Val Ala Lys Lys Val Gly  
 455 460

<210> 176  
 <211> 461  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 176  
 Met Trp Glu Arg Phe Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr  
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 Tyr Leu Tyr Phe Asp Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr  
 20 25 30  
 Gln Ala Thr Gly Leu Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys  
 35 40 45  
 Cys Trp Ala Gly Gly Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys  
 50 55 60  
 Thr Leu Leu Gly Gly Ala Ile Ser Val Thr Ile Gly His Leu Val Leu  
 65 70 75 80  
 Ala Gly Leu Gly Gly Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile  
 85 90 95  
 Ala Ile Gly Ser Gly Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly  
 100 105 110  
 Ser Arg His Gly Glu Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe  
 115 120 125  
 Gln Leu Phe Tyr Leu Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu  
 130 135 140  
 Leu Thr Gly Trp Leu Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly  
 145 150 155 160  
 Ala Ala Ala Val Leu Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu  
 165 170 175  
 Arg Lys Pro Met Leu Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu  
 180 185 190  
 Leu Arg Ala Gln Asn Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe  
 195 200 205  
 Ala Ala Val Ala Val Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr  
 210 215 220  
 Glu Thr Val Ser Ala Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr

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<211> 1647
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1624)  
<223> RXA02451
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taattggagt tgtgctttta ggtggaggat catagaggtt atg aac acc gac aca 115  
Met Asn Thr Asp Thr  
1 5

act caa gac ggt gtg agt cct gaa cct tcc gac ccc cac cta ggg tct 163  
 Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp Pro His Leu Gly Ser  
 10 15 20

gaa gtg gcg gaa act cac cgc gaa aag aaa ttc ttc ggc cag cct tgg 211  
 Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe Phe Gly Gln Pro Trp  
 25 30 35

ggg ctg gca aat ctc ttc ggc gtg gag atg tgg gag cga ttc agc ttc 259  
 Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp Glu Arg Phe Ser Phe  
 40 45 50

tac ggc atg cag tcc atc ctt gct ttc tat ctg tac tac tcc gtc acc 307  
 Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu Tyr Tyr Ser Val Thr  
 55 60 65

gat ggc gga ctt ggt atg aat cag aca gct gca ctg tcc att gtg ggc 355  
 Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala Leu Ser Ile Val Gly  
 70 75 80 85

gcc tac ggc ggc ttc gtc tac atg acc tcc ctc gtg gct tgc ttc att 403  
 Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu Val Ala Ser Phe Ile  
 90 95 100

gca gac cga gta ttg ggc tct gaa cgt aca ctc ttc tac tcc gcg atc 451  
 Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu Phe Tyr Ser Ala Ile  
 105 110 115

atc gtc atg ctg ggc cac att gcc ctg gcc ttg att ccg gga tat acg 499  
 Ile Val Met Leu Gly His Ile Ala Leu Ala Leu Ile Pro Gly Tyr Thr  
 120 125 130

gga ctg tcc atc ggc ttg gtc ctc atc ggc ctt ggc tca ggt ggc gtg 547  
 Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu Gly Ser Gly Gly Val  
 135 140 145

aag acg gca gcg cag gtt gtg ctg ggc cag ctg tac tca cgc acg gac 595  
 Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu Tyr Ser Arg Thr Asp  
 150 155 160 165

acg cgt cga gac gca ggc ttc tcc atc ttc tac atg ggc gtc aac ctc 643  
 Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr Met Gly Val Asn Leu  
 170 175 180

ggt ggc ctc ttt ggc ccg ctg atc acc aac gct ctg tgg gga tgg gga 691  
 Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala Leu Trp Gly Trp Gly  
 185 190 195

gga ttc cac tgg ggc ttc ggt atc gcc gca gtc ggc atg gct ttg ggt 739  
 Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val Gly Met Ala Leu Gly  
 200 205 210

ctc atc caa tac gtg gcg atg cgt aaa acc acc atc ggt gcg gca ggc 787  
 Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr Ile Gly Ala Ala Gly  
 215 220 225

cat act gtt cct aac cca ctg cct aag aat gaa tat gcg cgc tgg att 835  
 His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu Tyr Ala Arg Trp Ile  
 230 235 240 245

atc ggt gca gtc gtg gtt gtc gca gca gtt gtc gct ctc atc gca acg Ile Gly Ala Val Val Val Val Ala Ala Val Val Ala Leu Ile Ala Thr 250 255 260	883
ggc atc atc aag ctg gaa tgg ctg tcc aac atc acc gca gcg atc gca Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile Thr Ala Ala Ile Ala 265 270 275	931
ctg att gcg gct att gct ctg ctt gct cag atg tac gtt tcc cca ctg Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met Tyr Val Ser Pro Leu 280 285 290	979
acc acc gca gcg gaa aag tcc cgc ttg ttg gga ttc atc ccg atg ttc Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly Phe Ile Pro Met Phe 295 300 305	1027
atc ggt ggc gtg ctt ttc ttc gcg atc ttc caa acc cag ttc acg gtc Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln Thr Gln Phe Thr Val 310 315 320 325	1075
ctc gcg gtt tac tcc gac acc cgc ctg gac cgt aac ttc ttc ggc att Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg Asn Phe Phe Gly Ile 330 335 340	1123
gat ctt cct cca gga ttg atc aac tcc ttc aac cca atc ttc atc atc Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn Pro Ile Phe Ile Ile 345 350 355	1171
atc ttc tcc gga atc ttt gcc acc ttg tgg aca aaa ctc gga gca aag Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr Lys Leu Gly Ala Lys 360 365 370	1219
cag tgg tct act gca gtg aag ttc ggt gtc gcc aac att gtc att ggt Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala Asn Ile Val Ile Gly 375 380 385	1267
tgc gcg ctg ttc ttc ttc ctg ccg ttc gcc ggc ggt gca gag aac tct Cys Ala Leu Phe Phe Leu Pro Phe Ala Gly Gly Ala Glu Asn Ser 390 395 400 405	1315
acc cca atg gca ctg atc att tgg gtc tac ttc ctc ttc acc atc gct Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe Leu Phe Thr Ile Ala 410 415 420	1363
gag ctt ctg ctc tcc cct gtc ggc aac tca ctt gca acc aag gtc gca Glu Leu Leu Ser Pro Val Gly Asn Ser Leu Ala Thr Lys Val Ala 425 430 435	1411
ccc gag gca ttc cag tcc cgc atg ttc gcc gtg tgg ctg atg gct gtc Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val Trp Leu Met Ala Val 440 445 450	1459
tcc atg ggt acg tcc ctg tcc ggc acc ctg ggt ggt tac tac gat cca Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly Tyr Tyr Asp Pro 455 460 465	1507
acc gat gca gga tct gaa aag gtc ttc ttc att acc gtt ggc gtt gca Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile Thr Val Gly Val Ala 470 475 480 485	1555
gcc atc gtt ctt ggt gca atc gtc ata gca gcc aag ggc tgg gtg ctg	1603

Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala Lys Gly Trp Val Leu  
 490 495 500

aag aag ttc atc gac gtc cga taggcctcac aaagcctcaa aac  
 Lys Lys Phe Ile Asp Val Arg  
 505

1647

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 <211> 508  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 178  
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Pro His Leu Gly Ser Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe  
 20 25 30

Phe Gly Gln Pro Trp Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp  
 35 40 45

Glu Arg Phe Ser Phe Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu  
 50 55 60

Tyr Tyr Ser Val Thr Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala  
 65 70 75 80

Leu Ser Ile Val Gly Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu  
 85 90 95

Val Ala Ser Phe Ile Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu  
 100 105 110

Phe Tyr Ser Ala Ile Ile Val Met Leu Gly His Ile Ala Leu Ala Leu  
 115 120 125

Ile Pro Gly Tyr Thr Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu  
 130 135 140

Gly Ser Gly Gly Val Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu  
 145 150 155 160

Tyr Ser Arg Thr Asp Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr  
 165 170 175

Met Gly Val Asn Leu Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala  
 180 185 190

Leu Trp Gly Trp Gly Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val  
 195 200 205

Gly Met Ala Leu Gly Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr  
 210 215 220

Ile Gly Ala Ala Gly His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu  
 225 230 235 240

Tyr Ala Arg Trp Ile Ile Gly Ala Val Val Val Val Ala Ala Val Val  
 245 250 255

Ala Leu Ile Ala Thr Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile  
 260 265 270

Thr Ala Ala Ile Ala Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met  
 275 280 285

Tyr Val Ser Pro Leu Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly  
 290 295 300

Phe Ile Pro Met Phe Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln  
 305 310 315 320

Thr Gln Phe Thr Val Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg  
 325 330 335

Asn Phe Phe Gly Ile Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn  
 340 345 350

Pro Ile Phe Ile Ile Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr  
 355 360 365

Lys Leu Gly Ala Lys Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala  
 370 375 380

Asn Ile Val Ile Gly Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly  
 385 390 395 400

Gly Ala Glu Asn Ser Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe  
 405 410 415

Leu Phe Thr Ile Ala Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu  
 420 425 430

Ala Thr Lys Val Ala Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val  
 435 440 445

Trp Leu Met Ala Val Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly  
 450 455 460

Gly Tyr Tyr Asp Pro Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile  
 465 470 475 480

Thr Val Gly Val Ala Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala  
 485 490 495

Lys Gly Trp Val Leu Lys Lys Phe Ile Asp Val Arg  
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<210> 179  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (93)..(1403)  
 <223> RXA02394

<400> 179

tggtgatgaa tcagaagaac ctcgagattt ggacgagcta gaggcccaaaa gcgctataga	60
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Met Leu Ser Pro Ala Ala Val	
1 5	
gca gct tta att ctt gtc atc ggc att gtg gtg ctc atc atc gca tca	161
Ala Ala Leu Ile Leu Val Ile Gly Ile Val Val Leu Ile Ile Ala Ser	
10 15 20	
gtg ccc gtt gcc att gcc atc ggt ttg cca tca ctt ttt gcc gcg atg	209
Val Pro Val Ala Ile Ala Ile Gly Leu Pro Ser Leu Phe Ala Ala Met	
25 30 35	
gcc gtg ctt ggc cca gaa aac gcc gcg cag gcc gtc gcg cag cgc atg	257
Ala Val Leu Gly Pro Glu Asn Ala Ala Gln Ala Val Ala Gln Arg Met	
40 45 50 55	
ttt acc ggc aca aac tcc ttt aca ctc ctt gcc att ccg ttc ttc gtg	305
Phe Thr Gly Thr Asn Ser Phe Thr Leu Leu Ala Ile Pro Phe Phe Val	
60 65 70	
ttg gcg ggt ttg ctg atg aac tcg ggt ggt att gcc acg cgg ctt atc	353
Leu Ala Gly Leu Leu Met Asn Ser Gly Gly Ile Ala Thr Arg Leu Ile	
75 80 85	
gac gcc gcg aag gtg ctt gtc ggc cgc atg cct gcc tcc atg gcc aat	401
Asp Ala Ala Lys Val Leu Val Gly Arg Met Pro Ala Ser Met Ala Asn	
90 95 100	
acg aat atc gca gca aat ggt ctc ttc gga gca gtt tca ggg gca gcg	449
Thr Asn Ile Ala Ala Asn Gly Leu Phe Gly Ala Val Ser Gly Ala Ala	
105 110 115	
gta gca tca gct tct gcc gtg gga acc gtc atg aca cca aaa atg aag	497
Val Ala Ser Ala Ser Ala Val Gly Thr Val Met Thr Pro Lys Met Lys	
120 125 130 135	
gaa gag ggc tac tcg cgc gct tac gca gcg gcc gtc aac gtg gct tca	545
Glu Glu Gly Tyr Ser Arg Ala Tyr Ala Ala Val Asn Val Ala Ser	
140 145 150	
gca cct gcg ggc atg ctg atc ccg cca tca aac act ttt att gtg tat	593
Ala Pro Ala Gly Met Leu Ile Pro Pro Ser Asn Thr Phe Ile Val Tyr	
155 160 165	
tcc ttg gtg tcc tcg aca tca att gca gca cta ttt atg gcc ggt gtt	641
Ser Leu Val Ser Ser Thr Ser Ile Ala Ala Leu Phe Met Ala Gly Val	
170 175 180	
gga ccc ggt ctg ctc tgg att ctg gcc tgt gtc atc gtg gga act tgg	689
Gly Pro Gly Leu Leu Trp Ile Leu Ala Cys Val Ile Val Gly Thr Trp	
185 190 195	
tta gcg cga aag gaa aac tac aag cgc gag cag att cat cca aca ttc	737
Leu Ala Arg Lys Glu Asn Tyr Lys Arg Glu Gln Ile His Pro Thr Phe	
200 205 210 215	
aag cag tcg ctc gtt gtg ctg tgg agg gcg ctg cct tca ctg ctc atg	785
Lys Gln Ser Leu Val Val Leu Trp Arg Ala Leu Pro Ser Leu Leu Met	
220 225 230	



atc gtc att gtt gtt gga ggt atc ttg ctg ggc tgg ttc act cca act 833  
 Ile Val Ile Val Val Gly Gly Ile Leu Leu Gly Trp Phe Thr Pro Thr  
 235 240 245

gaa tcc gct got att gct gta gtg tac tgc ctg gtc ttg ggc ttt att 881  
 Glu Ser Ala Ala Ile Ala Val Val Tyr Cys Leu Val Leu Gly Phe Ile  
 250 255 260

tac cgc aca atc aag gtg gga gat ctg gca gat att ttg ctc aag gca 929  
 Tyr Arg Thr Ile Lys Val Gly Asp Leu Ala Asp Ile Leu Leu Lys Ala  
 265 270 275

act cgc acc aca tca att gtc atg ttg ctc att gca gtt tct gca gca 977  
 Thr Arg Thr Thr Ser Ile Val Met Leu Leu Ile Ala Val Ser Ala Ala  
 280 285 290 295

ctg tcg tgg gtg atg gcc ttt gcc aag atc cct cag atg atc tct gat 1025  
 Leu Ser Trp Val Met Ala Phe Ala Lys Ile Pro Gln Met Ile Ser Asp  
 300 305 310

gcg ctt ctt tcg gta tcc gat tcc aag gtt gtc atc ttg ttg atc atg 1073  
 Ala Leu Leu Ser Val Ser Asp Ser Lys Val Val Ile Leu Leu Ile Met  
 315 320 325

atg ttc atc ctg tta ctc atc ggt acc gta atg gac cca aca cca gca 1121  
 Met Phe Ile Leu Leu Leu Ile Gly Thr Val Met Asp Pro Thr Pro Ala  
 330 335 340

att ttg atc ttc gtc ccg atc ttc ctt cca gtg gtt acc gaa ctt ggt 1169  
 Ile Leu Ile Phe Val Pro Ile Phe Leu Pro Val Val Thr Glu Leu Gly  
 345 350 355

gtg gac cca gtc cac ttc ggt gcg atg gtg gta atg aac ctg tcc gtg 1217  
 Val Asp Pro Val His Phe Gly Ala Met Val Val Met Asn Leu Ser Val  
 360 365 370 375

ggc gtg att acc cca cca gta ggc aac gtg ttg ttc gtt ggt tcg caa 1265  
 Gly Val Ile Thr Pro Pro Val Gly Asn Val Leu Phe Val Gly Ser Gln  
 380 385 390

gtg gca ggg ctg cgt gtg gaa act gtg atc aga cga ctg tgg ccg tat 1313  
 Val Ala Gly Leu Arg Val Glu Thr Val Ile Arg Arg Leu Trp Pro Tyr  
 395 400 405

ctc att gcc att att gtt gcg ctg ttc gtg gtt gtt ttc gta ccg cag 1361  
 Leu Ile Ala Ile Ile Val Ala Leu Phe Val Val Val Phe Val Pro Gln  
 410 415 420

atc tct atc tgg ctg ccc aca aca atg gga ttg atg gga ggc 1403  
 Ile Ser Ile Trp Leu Pro Thr Thr Met Gly Leu Met Gly Gly  
 425 430 435

taaacctcca gccatcagct aag 1426

&lt;210&gt; 180

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 180

Met Leu Ser Pro Ala Ala Val Ala Ala Leu Ile Leu Val Ile Gly Ile  
 1 5 10 15  
 Val Val Leu Ile Ile Ala Ser Val Pro Val Ala Ile Ala Ile Gly Leu  
 20 25 30  
 Pro Ser Leu Phe Ala Ala Met Ala Val Leu Gly Pro Glu Asn Ala Ala  
 35 40 45  
 Gln Ala Val Ala Gln Arg Met Phe Thr Gly Thr Asn Ser Phe Thr Leu  
 50 55 60  
 Leu Ala Ile Pro Phe Phe Val Leu Ala Gly Leu Leu Met Asn Ser Gly  
 65 70 75 80  
 Gly Ile Ala Thr Arg Leu Ile Asp Ala Ala Lys Val Leu Val Gly Arg  
 85 90 95  
 Met Pro Ala Ser Met Ala Asn Thr Asn Ile Ala Ala Asn Gly Leu Phe  
 100 105 110  
 Gly Ala Val Ser Gly Ala Ala Val Ala Ser Ala Ser Ala Val Gly Thr  
 115 120 125  
 Val Met Thr Pro Lys Met Lys Glu Glu Gly Tyr Ser Arg Ala Tyr Ala  
 130 135 140  
 Ala Ala Val Asn Val Ala Ser Ala Pro Ala Gly Met Leu Ile Pro Pro  
 145 150 155 160  
 Ser Asn Thr Phe Ile Val Tyr Ser Leu Val Ser Ser Thr Ser Ile Ala  
 165 170 175  
 Ala Leu Phe Met Ala Gly Val Gly Pro Gly Leu Leu Trp Ile Leu Ala  
 180 185 190  
 Cys Val Ile Val Gly Thr Trp Leu Ala Arg Lys Glu Asn Tyr Lys Arg  
 195 200 205  
 Glu Gln Ile His Pro Thr Phe Lys Gln Ser Leu Val Val Leu Trp Arg  
 210 215 220  
 Ala Leu Pro Ser Leu Leu Met Ile Val Ile Val Val Gly Gly Ile Leu  
 225 230 235 240  
 Leu Gly Trp Phe Thr Pro Thr Glu Ser Ala Ala Ile Ala Val Val Tyr  
 245 250 255  
 Cys Leu Val Leu Gly Phe Ile Tyr Arg Thr Ile Lys Val Gly Asp Leu  
 260 265 270  
 Ala Asp Ile Leu Leu Lys Ala Thr Arg Thr Thr Ser Ile Val Met Leu  
 275 280 285  
 Leu Ile Ala Val Ser Ala Ala Leu Ser Trp Val Met Ala Phe Ala Lys  
 290 295 300  
 Ile Pro Gln Met Ile Ser Asp Ala Leu Leu Ser Val Ser Asp Ser Lys  
 305 310 315 320

Val Val Ile Leu Leu Ile Met Met Phe Ile Leu Leu Leu Ile Gly Thr  
 325 330 335

Val Met Asp Pro Thr Pro Ala Ile Leu Ile Phe Val Pro Ile Phe Leu  
 340 345 350

Pro Val Val Thr Glu Leu Gly Val Asp Pro Val His Phe Gly Ala Met  
 355 360 365

Val Val Met Asn Leu Ser Val Gly Val Ile Thr Pro Pro Val Gly Asn  
 370 375 380

Val Leu Phe Val Gly Ser Gln Val Ala Gly Leu Arg Val Glu Thr Val  
 385 390 395 400

Ile Arg Arg Leu Trp Pro Tyr Leu Ile Ala Ile Ile Val Ala Leu Phe  
 405 410 415

Val Val Val Phe Val Pro Gln Ile Ser Ile Trp Leu Pro Thr Thr Met  
 420 425 430

Gly Leu Met Gly Gly  
 435

<210> 181  
 <211> 1764  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1741)  
 <223> RXA01012

<400> 181  
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 Met Thr Thr Pro Leu  
 1 5

tta gag atc aac gat ctg gtt gtc tcc tat caa act gct aaa ggt ttg 163  
 Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln Thr Ala Lys Gly Leu  
 10 15 20

gtg cat gct gtc aac aat gtc agc ctg gag gtg cac cct ggc caa atc 211  
 Val His Ala Val Asn Asn Val Ser Leu Glu Val His Pro Gly Gln Ile  
 25 30 35

acc gcg att gtt ggt gag tcc ggt tct ggt aag tcc acc acc gct cag 259  
 Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Gln  
 40 45 50

gcc gtg att ggt ttg ctg gct gat aat gct gaa gtg gat tct ggt cgg 307  
 Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu Val Asp Ser Gly Arg  
 55 60 65

att tct ttc aac ggc cgt tcc ctt gtt ggc ttg aac gca cgt gag tgg 355  
 Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu Asn Ala Arg Glu Trp  
 70 75 80 85

aaa aac gtt cgc ggt acc aaa att ggt ttg att ccg cag gac ccc aac 403  
 Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile Pro Gln Asp Pro Asn  
 90 95 100

aac tct ctg aac ccg gtg aaa act atc ggc gct tca gtg ggg gag ggc 451  
 Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala Ser Val Gly Glu Gly  
 105 110 115

ttg gct atc cac aag cgt gga acc gcc gcc gag cgc aaa aag aag gtc 499  
 Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu Arg Lys Lys Lys Val  
 120 125 130

att gag ctt cta gag cgc gtg ggt att gat aac cca gag gtc cgc tat 547  
 Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn Pro Glu Val Arg Tyr  
 135 140 145

gac cag tac ccg cat gag ctg tct ggt ggc atg aag cag cgc gcg ttg 595  
 Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met Lys Gln Arg Ala Leu  
 150 155 160 165

att gcc gct gcc att gca ctt gaa cca gag ctg atc att gcc gat gag 643  
 Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu Ile Ile Ala Asp Glu  
 170 175 180

ccc aca tct gcg ctg gat gtg acc gtg cag aaa att att ctc gat ctg 691  
 Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys Ile Ile Leu Asp Leu  
 185 190 195

ctg gaa gac atg cag cgt gaa ttg ggc atg ggt att ttg ttc att act 739  
 Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly Ile Leu Phe Ile Thr  
 200 205 210

cac gat cta gcc gtg gca ggc gat cgg gcg gat cgc atc gtc gtc atg 787  
 His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp Arg Ile Val Val Met  
 215 220 225

caa aaa ggc gag gtg cgc gaa agt ggt tac gcg gct tcg gtc ttg acc 835  
 Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala Ala Ser Val Leu Thr  
 230 235 240 245

gac ccc cag cat gag tat tcc aag aag ttg ctt gcc gac gcg ccc tcc 883  
 Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu Ala Asp Ala Pro Ser  
 250 255 260

ctc acc atc ggc gag atc ccc acg cga gtt ccg gcc gta gat ccg gag 931  
 Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro Ala Val Asp Pro Glu  
 265 270 275

gta gcg cag gcc aaa ggc ccg ctt ctg gta gtg gat aaa ttc cgc aag 979  
 Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val Asp Lys Phe Arg Lys  
 280 285 290

gaa cac caa cga ggc aaa gaa gga gca ttt gtt gcc gca aat gat att 1027  
 Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val Ala Ala Asn Asp Ile  
 295 300 305

tcc ttc gaa gta ctg cct ggc acc acg cat gcc atc gtc ggt gaa tcc 1075  
 Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala Ile Val Gly Glu Ser  
 310 315 320 325

ggt tct ggt aaa acc acg ctt ggc cgc gcg atc gcg atg ttt aat acg 1123  
 Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile Ala Met Phe Asn Thr  
 330 335 340

ccg acc tct ggt tcc att tca gta agt ggc aag gac atc acc aac ctg 1171  
 Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys Asp Ile Thr Asn Leu  
 345 350 355

tcc aag gcc cag cag cgg gaa ctg cgc cag caa atc cag ctg gtg tac 1219  
 Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln Ile Gln Leu Val Tyr  
 360 365 370

caa aac ccg tat tct tcc ctg gat cct cgc caa acc att ggc tcc acc 1267  
 Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln Thr Ile Gly Ser Thr  
 375 380 385

atc gcg gaa cct ctg cgc aat ttc acc aag gtg agc aag cag gaa gcc 1315  
 Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val Ser Lys Gln Glu Ala  
 390 395 400 405

gac gaa aag gtg gca cac tac ctg gaa ctg gtg gcg ctt gac ccg gct 1363  
 Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val Ala Leu Asp Pro Ala  
 410 415 420

ctt gcc acc cgt cgc cca cgt gag ctc tct ggt ggt cag cgc cag cgc 1411  
 Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly Gly Gln Arg Gln Arg  
 425 430 435

gtc gcc att gct cgt gcc atg att ttg gaa cct gaa ttg gtg gtt ttc 1459  
 Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro Glu Leu Val Val Phe  
 440 445 450

gac gaa gcc gta tcc gcg ttg gat gtg act gtg cag gca caa atc ctg 1507  
 Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val Gln Ala Gln Ile Leu  
 455 460 465

cgc ctg ctc gac gat ctg caa cga gag cta ggc ttg act tac gtg ttt 1555  
 Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly Leu Thr Tyr Val Phe  
 470 475 480 485

att tcc cac gac ctg gct gtg gtc cgt gaa atc tct gac act gtg tct 1603  
 Ile Ser His Asp Leu Ala Val Val Arg Glu Ile Ser Asp Thr Val Ser  
 490 495 500

gtg atg agt cgc ggc aac cag gtg gaa ctt gga aaa acc gca gaa gta 1651  
 Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly Lys Thr Ala Glu Val  
 505 510 515

ttt aac aac ccg caa acc gat ttc act cgc cga ctc atc gac gcg atc 1699  
 Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg Leu Ile Asp Ala Ile  
 520 525 530

cca gga tcg cgc tat cgt ggt ggc gaa ctc aat ctt gga cta 1741  
 Pro Gly Ser Arg Tyr Arg Gly Glu Leu Asn Leu Gly Leu  
 535 540 545

taggagcaga tcttaaaaat gtc 1764

&lt;210&gt; 182

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 182

Met Thr Thr Pro Leu Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln  
 1 5 10 15  
 Thr Ala Lys Gly Leu Val His Ala Val Asn Asn Val Ser Leu Glu Val  
 20 25 30  
 His Pro Gly Gln Ile Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys  
 35 40 45  
 Ser Thr Thr Ala Gln Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu  
 50 55 60  
 Val Asp Ser Gly Arg Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu  
 65 70 75 80  
 Asn Ala Arg Glu Trp Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile  
 85 90 95  
 Pro Gln Asp Pro Asn Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala  
 100 105 110  
 Ser Val Gly Glu Gly Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu  
 115 120 125  
 Arg Lys Lys Lys Val Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn  
 130 135 140  
 Pro Glu Val Arg Tyr Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met  
 145 150 155 160  
 Lys Gln Arg Ala Leu Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu  
 165 170 175  
 Ile Ile Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys  
 180 185 190  
 Ile Ile Leu Asp Leu Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly  
 195 200 205  
 Ile Leu Phe Ile Thr His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp  
 210 215 220  
 Arg Ile Val Val Met Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala  
 225 230 235 240  
 Ala Ser Val Leu Thr Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu  
 245 250 255  
 Ala Asp Ala Pro Ser Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro  
 260 265 270  
 Ala Val Asp Pro Glu Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val  
 275 280 285  
 Asp Lys Phe Arg Lys Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val  
 290 295 300

Ala Ala Asn Asp Ile Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala  
 305 310 315 320  
 Ile Val Gly Glu Ser Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile  
 325 330 335  
 Ala Met Phe Asn Thr Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys  
 340 345 350  
 Asp Ile Thr Asn Leu Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln  
 355 360 365  
 Ile Gln Leu Val Tyr Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln  
 370 375 380  
 Thr Ile Gly Ser Thr Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val  
 385 390 395 400  
 Ser Lys Gln Glu Ala Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val  
 405 410 415  
 Ala Leu Asp Pro Ala Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly  
 420 425 430  
 Gly Gln Arg Gln Arg Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro  
 435 440 445  
 Glu Leu Val Val Phe Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val  
 450 455 460  
 Gln Ala Gln Ile Leu Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly  
 465 470 475 480  
 Leu Thr Tyr Val Phe Ile Ser His Asp Leu Ala Val Val Arg Glu Ile  
 485 490 495  
 Ser Asp Thr Val Ser Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly  
 500 505 510  
 Lys Thr Ala Glu Val Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg  
 515 520 525  
 Leu Ile Asp Ala Ile Pro Gly Ser Arg Tyr Arg Gly Gly Glu Leu Asn  
 530 535 540  
 Leu Gly Leu  
 545

&lt;210&gt; 183

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(739)

&lt;223&gt; RXA02660

&lt;400&gt; 183

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<210> 184



<211> 213  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 184  
 Met Ile Ile Gly Val Thr Leu Leu Val Phe Ile Val Met Ser Phe Ser  
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 Pro Ala Asp Pro Ala Arg Leu Ala Leu Gly Glu Ser Ala Ser Pro Glu  
 20 25 30  
 Ala Leu Glu Ala Tyr Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met  
 35 40 45  
 Val Arg Tyr Phe Asp Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly  
 50 55 60  
 Thr Ser Ser Gly Gly Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe  
 65 70 75 80  
 Pro Ile Thr Leu Gln Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val  
 85 90 95  
 Val Ala Leu Ile Leu Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp  
 100 105 110  
 Pro Asp Gln Leu Ile Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro  
 115 120 125  
 Ser Phe Trp Leu Ala Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro  
 130 135 140  
 Gly Ala Trp Gly Phe Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe  
 145 150 155 160  
 Ser Glu Asp Pro Ala Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu  
 165 170 175  
 Arg Trp Gln Ser Pro Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro  
 180 185 190  
 Pro Trp Trp Lys Asn Trp Thr Arg Thr Thr Ser Ala Gln Gln Ser Val  
 195 200 205  
 Gln Asp Pro Gln Asn  
 210

<210> 185  
 <211> 342  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(319)  
 <223> RXA02661

<400> 185  
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ccgcaatggtt ctgcgcaatg cgctgatcac cccaatcacc gtg att ggt ctt cgc 115  
 Val Ile Gly Leu Arg  
 1 5

gtt ggt tcc ctc atg ggt ggt gcg gtg atc att gag atc atc ttc aac 163  
 Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile Glu Ile Ile Phe Asn  
 10 15 20

atc caa gca atg gga cag ctc atc cta gac ggt gtg acc cga aat gac 211  
 Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly Val Thr Arg Asn Asp  
 25 30 35

gtc tac ctc gtc caa ggt gtc acc ctc acc gtt gcc atc gcc ttc atc 259  
 Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val Ala Ile Ala Phe Ile  
 40 45 50

atc gtc aat atc gcc gtg gac ctg ctc tac gtc ctg gtc aat cca cgt 307  
 Ile Val Asn Ile Ala Val Asp Leu Leu Tyr Val Leu Val Asn Pro Arg  
 55 60 65

att agg agc atc tagatgcgcc gtaaaactaac cac 342  
 Ile Arg Ser Ile  
 70

<210> 186

<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Val Ile Gly Leu Arg Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile  
 1 5 10 15

Glu Ile Ile Phe Asn Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly  
 20 25 30

Val Thr Arg Asn Asp Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val  
 35 40 45

Ala Ile Ala Phe Ile Ile Val Asn Ile Ala Val Asp Leu Leu Tyr Val  
 50 55 60

Leu Val Asn Pro Arg Ile Arg Ser Ile  
 65 70

<210> 187

<211> 1089

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1066)

<223> RXA02034

<400> 187

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aattgtcgtt gattggtcgg aaagaatccg gggtagcgca gtg agt aaa aca atc 115

	Val	Ser	Lys	Thr	Ile	
	1				5	
gct tgg act gtg ctg cgg tac acc ctg act ttt gtg atc gcc agc atc Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe Val Ile Ala Ser Ile	10			15	20	163
atc att ttt gtg ctg att cga gtc atc ccc ggt gac ccc gcc gct gtt Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly Asp Pro Ala Ala Val	25			30	35	211
gcc ctg gga att acc gcg aca cca gaa gca atc gct gcg ttg caa tca Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile Ala Ala Leu Gln Ser	40			45	50	259
caa tta ggt act gat caa ccg ctt ttc caa cag tac ttt tcc tgg ata Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln Tyr Phe Ser Trp Ile	55			60	65	307
ggt gga atg ctc act ggc gat ttc ggc acc tcg ctg agc tct ggc caa Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser Leu Ser Ser Gly Gln	70			75	80	355
gac ctt tcc ccc atc att ttt gac cgc tta caa gtg agc ctc att ttg Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln Val Ser Leu Ile Leu	90			95	100	403
gtg gga tgc tcc att gtg ttg tcg ttg ctc att gcc att cca ctt ggt Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile Ala Ile Pro Leu Gly	105			110	115	451
gtg ctt tcg gcc cgg cgc ggt ggc gtg atc att tcc ggc atc agc cag Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile Ser Gly Ile Ser Gln	120			125	130	499
att ggc att gcg atc cct agt ttc ctc gcc ggt att ttg ttg gtc gct Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly Ile Leu Leu Val Ala	135			140	145	547
gtc ttc gcc gtt ggt ttg ggg tgg ctg ccc gcc aat ggc tgg att ccg Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala Asn Gly Trp Ile Pro	150			155	160	595
ccg tcg gaa aac ttt gga ggt ttc tta gcc agg ctg atc ctc ccg gtt Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg Leu Ile Leu Pro Val	170			175	180	643
ctg gct ctt act gct gtt caa gca gca att ttg acc cgc tat gtc cgc Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu Thr Arg Tyr Val Arg	185			190	195	691
tct gca gta atg gat gta atg ggg caa gat ttc atg cgc acc gcg agg Ser Ala Val Met Asp Val Met Gly Gln Asp Phe Met Arg Thr Ala Arg	200			205	210	739
tcg aaa ggt atg agc ttc aac cgc gcg ttg atc atc cac ggt ctt cgg Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile Ile His Gly Leu Arg	215			220	225	787
aat gct gct ctt cct gtc ctt acc gtc act ggt ttg cag cta aca acc Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly Leu Gln Leu Thr Thr						835

230	235	240	245	
ttg gtt atc ggc gcc gtg gtg att gaa caa gtc ttt gtc atc ccc gga				883
Leu Val Ile Gly Ala Val Val Ile Glu Gln Val Phe Val Ile Pro Gly				
250		255	260	
atc ggt tgc atg ctg ctg gag tcc gtg tcc aac cgt gat ctc atc gct				931
Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn Arg Asp Leu Ile Ala				
265		270	275	
gtg caa tct att gtc atg ctg ctg gtg gcg ttc acg ttg ctg gtt aat				979
Val Gln Ser Ile Val Met Leu Leu Val Ala Phe Thr Leu Leu Val Asn				
280		285	290	
ttg gtg gtt gat ctg ctg tat cag gtg gtt gat cca aga gtc ggt gct				1027
Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp Pro Arg Val Gly Ala				
295		300	305	
gtt ggg gtt gct agc act aag gtt cca ggg agc gtg gct taagtgacaa				1076
Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser Val Ala				
310		315	320	
cgatcaaaaa cat				1089

<210> 188  
 <211> 322  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 188  
 Val Ser Lys Thr Ile Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe  
 1 5 10 15  
 Val Ile Ala Ser Ile Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly  
 20 25 30  
 Asp Pro Ala Ala Val Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile  
 35 40 45  
 Ala Ala Leu Gln Ser Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln  
 50 55 60  
 Tyr Phe Ser Trp Ile Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser  
 65 70 75 80  
 Leu Ser Ser Gly Gln Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln  
 85 90 95  
 Val Ser Leu Ile Leu Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile  
 100 105 110  
 Ala Ile Pro Leu Gly Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile  
 115 120 125  
 Ser Gly Ile Ser Gln Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly  
 130 135 140  
 Ile Leu Leu Val Ala Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala  
 145 150 155 160

Asn Gly Trp Ile Pro Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg  
 165 170 175  
 Leu Ile Leu Pro Val Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu  
 180 185 190  
 Thr Arg Tyr Val Arg Ser Ala Val Met Asp Val Met Gly Gln Asp Phe  
 195 200 205  
 Met Arg Thr Ala Arg Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile  
 210 215 220  
 Ile His Gly Leu Arg Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly  
 225 230 235 240  
 Leu Gln Leu Thr Thr Leu Val Ile Gly Ala Val Val Ile Glu Gln Val  
 245 250 255  
 Phe Val Ile Pro Gly Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn  
 260 265 270  
 Arg Asp Leu Ile Ala Val Gln Ser Ile Val Met Leu Leu Val Ala Phe  
 275 280 285  
 Thr Leu Leu Val Asn Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp  
 290 295 300  
 Pro Arg Val Gly Ala Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser  
 305 310 315 320  
 Val Ala

<210> 189  
 <211> 818  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(795)  
 <223> RXA01013

<400> 189  
 ttg ggc aat cct tgg acg agg cct gct gct gtt att tcc atc gtg gta 48  
 Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val  
 1 5 10 15  
 ctc gcc gtt gcg gtg ctg atg gca ctt gtt cct gga ctg ttt acc tcc 96  
 Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser  
 20 25 30  
 cag gat ccg ttc act ggc gat gat gtg gcg ctg ctt ggg cca agt ggc 144  
 Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly  
 35 40 45  
 acc cac tgg ttt ggt acc gat tcc gtg gga cgc gat ctc tac agt cgt 192  
 Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg  
 50 55 60

gtt gtt tac ggc gcg agg gaa acc ctg ctc ggt gca ctg atc gca gtg 240  
 Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val  
 65 70 75 80

ctg gtt ggt ctg atc gtg gga acc ctg atc gga ctg ctc gca ggt gca 288  
 Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala  
 85 90 95

cag cgc ggt tgg gtt gac act gta tta atg cgt ttc gtg gat gtg ctg 336  
 Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu  
 100 105 110

ttg tcc atc ccg gca ctg ctg ctc agc ttg act gtc att atc ctt ttg 384  
 Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu  
 115 120 125

gga ttc ggc acc atg aac gca gcg atc gca gtc ggt att acc tct gtt 432  
 Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val  
 130 135 140

gcc acc ttc gcg cgt ctg gcg cgt tcc cag gtg atg act gtt gca ggt 480  
 Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly  
 145 150 155 160

tcc gat ttc gtg gaa gct gca tac ggt tcc ggt ggc acc cag gcg cag 528  
 Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln  
 165 170 175

gtg ttg ttc cgc cac att ctg cct aac tct ctg acc cca gtg ttt gct 576  
 Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala  
 180 185 190

ctt gca gca ctg cag ttc ggt tcc gcg att ttg cag ctg tcc gtg ttg 624  
 Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu  
 195 200 205

ggc ttc ttg ggc tac ggc gct ccg gca cca aca cca gag tgg ggt ctg 672  
 Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu  
 210 215 220

ctg atc tct gat gcc cgc gac tac atg gcg acc tca tgg tgg ctg act 720  
 Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr  
 225 230 235 240

gtg ctg cct ggt ttt gtc atc atc gcc gtg gtt atg tct gcc aac tac 768  
 Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr  
 245 250 255

cta agc cgc atc att cag aag gag gca tagaaaaatga ctactccctt gtt 818  
 Leu Ser Arg Ile Ile Gln Lys Glu Ala  
 260 265

&lt;210&gt; 190

&lt;211&gt; 265

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 190

Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val  
 1 5 10 15

Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser  
                   20                                  25                                  30  
 Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly  
                   35                                  40                                  45  
 Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg  
                   50                                  55                                  60  
 Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val  
                   65                                  70                                  75                                  80  
 Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala  
                                   85                                  90                                  95  
 Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu  
                                   100                                  105                                  110  
 Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu  
                   115                                  120                                  125  
 Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val  
                   130                                  135                                  140  
 Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly  
                   145                                  150                                  155                                  160  
 Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln  
                                   165                                  170                                  175  
 Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala  
                                   180                                  185                                  190  
 Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu  
                   195                                  200                                  205  
 Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu  
                   210                                  215                                  220  
 Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr  
                   225                                  230                                  235                                  240  
 Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr  
                                   245                                  250                                  255  
 Leu Ser Arg Ile Ile Gln Lys Glu Ala  
                   260                                  265

&lt;210&gt; 191

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(910)

&lt;223&gt; RXN02933

&lt;400&gt; 191

tgatctgctg	tatcaggtgg	ttgatccaag	agtcggtgct	gttggggttg	ctagcactaa	60
ggttccaggg	agcgtggctt	aagtgacaac	gatcaaaaac	atg ccc ctt tca ggg	115	
				Met Pro Leu Ser Gly	5	
				1		
aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg	163					
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu						
	10			15	20	
tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag	211					
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu						
	25			30	35	
cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat	259					
Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr						
	40			45	50	
ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg	307					
Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu						
	55			60	65	
ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca	355					
Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro						
	70			75	80	
ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc	403					
Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val						
	90			95	100	
atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg	451					
Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala						
	105			110	115	
att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc	499					
Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val						
	120			125	130	
gcg atc ggc atc gca gcc atc cct agt ttt gcc cgc gtg gct cgt gca	547					
Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala						
	135			140	145	
ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta	595					
Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu						
	150			155	160	
tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac	643					
Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn						
	170			175	180	
atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg	691					
Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala						
	185			190	195	
atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc	739					
Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro						
	200			205	210	
ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc	787					
Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile						
	215			220	225	



ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg 835  
 Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu  
 230 235 240 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc 883  
 Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile  
 250 255 260

gat cca aag cgg gag gtc ggc cgt gct taaagtttct gatttaacgg ttg 933  
 Asp Pro Lys Arg Glu Val Gly Arg Ala  
 265 270

<210> 192

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 192

Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe  
 1 5 10 15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln  
 20 25 30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu  
 35 40 45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly  
 50 55 60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala  
 65 70 75 80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met  
 85 90 95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro  
 100 105 110

Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr  
 115 120 125

Trp Ser Ala Met Val Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala  
 130 135 140

Arg Val Ala Arg Ala Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile  
 145 150 155 160

Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg  
 165 170 175

His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val  
 180 185 190

Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly  
 195 200 205

Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr  
 210 215 220

Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly  
 225 230 235 240

Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly  
 245 250 255

Leu Arg Asp Ala Ile Asp Pro Lys Arg Glu Val Gly Arg Ala  
 260 265 270

<210> 193  
 <211> 900  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(889)  
 <223> FRXA02033

<400> 193  
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 ggttccaggg agcgtggctt aagtgacaac gatcaaaaac atg ccc ctt tca ggg 115  
 Met Pro Leu Ser Gly  
 1 5  
 aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163  
 Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu  
 10 15 20  
 tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211  
 Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu  
 25 30 35  
 cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat 259  
 Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr  
 40 45 50  
 ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg 307  
 Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu  
 55 60 65  
 ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca 355  
 Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro  
 70 75 80 85  
 ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc 403  
 Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val  
 90 95 100  
 atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg 451  
 Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala  
 105 110 115  
 att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc 499  
 Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val  
 120 125 130  
 gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca 547

Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala  
 135 140 145

ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta 595  
 Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu  
 150 155 160 165

tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac 643  
 Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn  
 170 175 180

atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg 691  
 Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala  
 185 190 195

atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc 739  
 Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro  
 200 205 210

ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc 787  
 Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile  
 215 220 225

ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg 835  
 Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu  
 230 235 240 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc 883  
 Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile  
 250 255 260

gat cca tagtattata t 900  
 Asp Pro

<210> 194  
 <211> 263  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 194  
 Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe  
 1 5 10 15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln  
 20 25 30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu  
 35 40 45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly  
 50 55 60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala  
 65 70 75 80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met  
 85 90 95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro

100	105	110
Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr		
115	120	125
Trp Ser Ala Met Val Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala		
130	135	140
Arg Val Ala Arg Ala Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile		
145	150	155
Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg		
165	170	175
His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val		
180	185	190
Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly		
195	200	205
Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr		
210	215	220
Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly		
225	230	235
Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly		
245	250	255
Leu Arg Asp Ala Ile Asp Pro		
260		

<210> 195  
 <211> 958  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> RXA01006

<400> 195  
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 cattgaccat tccagcgacc attccagtga ggaggactaa atg act acc tcg cag 115  
 Met Thr Thr Ser Gln  
 1 5  
 att ctg cgc cgc atc ggc caa gcc gtc ttg gtc ttg ttg gtc acc ttt 163  
 Ile Leu Arg Arg Ile Gly Gln Ala Val Leu Val Leu Leu Val Thr Phe  
 10 15 20  
 acc ttg gcg ttc atc atg ctt tcc gcc ctc cct ggc gat gct gtg tcc 211  
 Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro Gly Asp Ala Val Ser  
 25 30 35  
 gcc cgc tat tcc agc cct gat ttg ggt ctg tca cct gag cag atc gca 259  
 Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser Pro Glu Gln Ile Ala  
 40 45 50

cag atc cgt gaa tcc tat ggt gcc gat gaa tcc ctg atc gct cag tac 307  
 Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser Leu Ile Ala Gln Tyr  
 55 60 65

ttc tcc acc ttg ggt ggc ttc ctt gta ggt aac ttc ggt tac tcc gta 355  
 Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn Phe Gly Tyr Ser Val  
 70 75 80 85

caa acc gga act gcc gtg gca acc cag ctg gca gaa gcc cta cca ggc 403  
 Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala Glu Ala Leu Pro Gly  
 90 95 100

acc ttg acc ttg gct att ttg gca ttc ttg ctc gca gcc att ttg gca 451  
 Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu Ala Ala Ile Leu Ala  
 105 110 115

ctg gtt att tcc att ctt gcc acc atg gat cgc ttt gca tgg atc aag 499  
 Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg Phe Ala Trp Ile Lys  
 120 125 130

ggc atc ttc cag gct ctg cct cca ttc ttt gtg tcc ctt cca agt ttc 547  
 Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val Ser Leu Pro Ser Phe  
 135 140 145

tgg ttg ggc atc atc ttg atc cag atc gtg tcc ttc cgc ctt ggt tgg 595  
 Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser Phe Arg Leu Gly Trp  
 150 155 160 165

gtc ccc gtt att ggg acc acc ccg gca caa gga ctg atc ctg ccg acc 643  
 Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly Leu Ile Leu Pro Thr  
 170 175 180

atc acc ttg tcc atc cca att acc gct ccg ctt gca cag gtg ctc atc 691  
 Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu Ala Gln Val Leu Ile  
 185 190 195

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 Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe Ile Ala Ala Val Arg  
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 Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe Arg Asn Ile Ile Arg  
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cta gtc ggt ggg gcc gtg gtc acc gag gca gtg ttc ggc cgc gct gga 883  
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ctt ggc caa atg acc gtc aac gca gtg gcc aac cgc gat atg cca gtg 931  
 Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn Arg Asp Met Pro Val  
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 Phe Gly Tyr Ser Val Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala  
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 Glu Ala Leu Pro Gly Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu  
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 Ala Ala Ile Leu Ala Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg  
                   115                  120                  125  
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 Ser Leu Pro Ser Phe Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser  
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 Phe Arg Leu Gly Trp Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly  
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 Ala Gln Val Leu Ile Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe  
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 Arg Asn Ile Ile Arg Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly  
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 Ile Leu Phe Gly Glu Leu Val Gly Gly Ala Val Val Thr Glu Ala Val  
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 Phe Gly Arg Ala Gly Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn  
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 Arg Asp Met Pro Val Met Leu Ala Ile Val Val Ile Ala Ala  
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Leu Ser Asn Arg His																	
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Leu Phe Gly Glu Met Glu Phe Trp Phe Ala Ile Ile Lys Ile Val Ala																	
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Ile Val Ser Leu Ile Val Val Gly Leu Phe Met Val Val Thr Ala Phe																	
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 Gly Gly Phe Phe Pro Asn Gly Ile Thr Gly Phe Leu Ala Gly Phe Gln  
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 Ile Ala Ile Phe Ala Phe Val Gly Ile Glu Leu Ala Gly Thr Ala Ala  
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gca gag act gag aat ccc acc aag acg ctt cct cgg gca atc aac tcc 787  
 Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro Arg Ala Ile Asn Ser  
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 Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu Ala Leu Ala Val Ile  
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atg atg gtc acc cca tgg gat cag gtc cgt gct gac aac agc cca ttc 883  
 Met Met Val Thr Pro Trp Asp Gln Val Arg Ala Asp Asn Ser Pro Phe  
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 Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala Ala Ala Gly Ile Ile  
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 Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser Leu Glu Gly Ala Ala  
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 Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu Val Pro Ala Arg Gly  
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tcg gtg ttg ttc atg gtg gtg tgg tcc tac att ttg gtg gct tat atc 1219  
 Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile Leu Val Ala Tyr Ile  
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 Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys Lys Ser Ile Phe Lys  
 375 380 385

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 Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp Thr Arg Ala Ala Leu  
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ser val ile leu val tyr ala ile ile gly phe met leu phe phe val  
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met arg ala met gly glu leu leu leu ala asn leu asn tyr lys ser  
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leu arg asp ala val ser asp ile leu gly pro gly ala gly phe val  
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thr gly trp thr tyr trp phe cys trp ile ala thr gly met ala asp  
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ile val ala ile thr gly tyr thr gln tyr trp trp pro glu ile pro  
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leu trp leu pro gly val leu thr ile ala leu leu phe ala leu asn  
                   115                                  120                                  125

leu ala ala val arg leu phe gly glu met glu phe trp phe ala ile  
                   130                                  135                                  140

ile lys ile val ala ile val ser leu ile val val gly leu phe met  
                   145                                  150                                  155                                  160

val val thr ala phe glu ser pro asn gly thr thr ala gln phe asn  
                                   165                                  170                                  175

asn leu ile glu his gly gly phe phe pro asn gly ile thr gly phe  
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leu ala gly phe gln ile ala ile phe ala phe val gly ile glu leu  
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ala gly thr ala ala ala glu thr glu asn pro thr lys thr leu pro  
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arg ala ile asn ser ile pro ile arg ile val val phe tyr val leu  
                   225                                  230                                  235                                  240

Ala Leu Ala Val Ile Met Met Val Thr Pro Trp Asp Gln Val Arg Ala  
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Asp Asn Ser Pro Phe Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala  
 260 265 270

Ala Ala Gly Ile Ile Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser  
 275 280 285

Ala Asn Ser Gly Ile Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser  
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Leu Glu Gly Ala Ala Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu  
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Val Pro Ala Arg Gly Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala  
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Val Gly Leu Leu Tyr Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu  
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Ile Thr Thr Val Ser Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile  
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Leu Val Ala Tyr Ile Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys  
 370 375 380

Lys Ser Ile Phe Lys Met Pro Gly Gly Val Val Met Ala Val Val Val  
 385 390 395 400

Leu Val Phe Phe Ala Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp  
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Thr Arg Ala Ala Leu Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly  
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 Val Ala Val Asp Lys

1 5

gat att gaa aac cgc acc tca gac ctt tct cga tgg gaa act atg gag 163  
 Asp Ile Glu Asn Arg Thr Ser Asp Leu Ser Arg Trp Glu Thr Met Glu  
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 Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val Phe Phe Phe Gly Ala  
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 Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr Thr Trp Leu Leu Ser  
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gga aaa cgc ggc gat atg cac gcc atg ctg ctt gtc ggc atc atc att 691  
 Gly Lys Arg Gly Asp Met His Ala Met Leu Leu Val Gly Ile Ile Ile  
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ggt ggc gga ctc gga tcc atc tcc acc ttt atg cag cgc att ctg acc 739  
 Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met Gln Arg Ile Leu Thr  
 200 205 210

cca tca gaa ttc gat att ctt tcc gcc cga ctt ttc gga tca gta aac 787  
 Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu Phe Gly Ser Val Asn  
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 Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val Pro Leu Val Val Val  
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 265 270 275

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gca tat caa ttc gcc gac act tac gac cac cga tac atc ctt ccg atg 1075  
 Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg Tyr Ile Leu Pro Met  
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&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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 35 40 45

Thr Ala Arg Ala Lys Arg Arg Tyr Trp Ile Ile Met Ala Ala Leu Leu  
 50 55 60

Val Thr Ala Leu Ala Phe Thr Trp Gly Leu Ile Trp Tyr Lys Asn Pro  
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Met Pro Val Gly His Pro Ala Phe Ala Leu Ile Ala Glu Arg Arg Met  
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Glu Ser Val Phe Val Met Leu Ile Val Ala Val Cys Gln Gly Phe Ala  
 100 105 110

Thr Val Ala Phe Gln Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser  
 115 120 125  
 Ile Met Gly Phe Glu Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val  
 130 135 140  
 Phe Phe Phe Gly Ala Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met  
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 Phe Val Gly Gln Leu Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr  
 165 170 175  
 Thr Trp Leu Leu Ser Gly Lys Arg Gly Asp Met His Ala Met Leu Leu  
 180 185 190  
 Val Gly Ile Ile Ile Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met  
 195 200 205  
 Gln Arg Ile Leu Thr Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu  
 210 215 220  
 Phe Gly Ser Val Asn Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val  
 225 230 235 240  
 Pro Leu Val Val Val Ala Ser Val Leu Leu Leu Leu Ser Ser Arg Arg  
 245 250 255  
 Leu Asn Val Val Gly Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile  
 260 265 270  
 Asn His Arg Arg Ser Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu  
 275 280 285  
 Met Ala Val Ser Thr Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe  
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 Leu Val Ala Thr Leu Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg  
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 Tyr Ile Leu Pro Met Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly  
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 Ala Tyr Phe Val Met Asn His Val Phe Arg Ala Gln Gly Val Val Ser  
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	Met Ala Thr Pro Ala 1 5
tgc gct ccc act tcc gaa cca cgt ctg aaa cgc acc aga gcc aag ctt	163
Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg Thr Arg Ala Lys Leu	10 15 20
ttt gat tgg aag ctt ctg atc ggc atc att ttg gtc gcc ggc ctg gtg	211
Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe Val Ala Gly Leu Val	25 30 35
gtg ctt tcc ctg ctg acc ggc caa tac gac att ttg ggt ggc gat gat	259
Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile Phe Gly Gly Asp Asp	40 45 50
ggc caa ctg atg ttg gag gca gtt cgc atc ccg cgt acc gtt tcc ctg	307
Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro Arg Thr Val Ser Leu	55 60 65
att ttg tcc ggt gca gca atg gcg atg tgt ggc tta gtc atg cag ctg	355
Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly Leu Val Met Gln Leu	70 75 80 85
ttg acc caa aac aaa ttg gtg gaa ccc agc acc aca gga aca acc gaa	403
Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr Thr Gly Thr Thr Glu	90 95 100
tgg gca ggt ctt ggc ctg ctg ttg gtg att tac ttg gtg cca gcc gcg	451
Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr Phe Val Pro Ala Ala	105 110 115
acc gtt ttg gat cgc atg ctg ggt gcc gtg gtg ttt tcc ttg atc gga	499
Thr Val Leu Asp Arg Met Leu Gly Ala Val Val Phe Ser Phe Ile Gly	120 125 130
acc atg gtg ttg ttg ctg ttg ttg cta cgc cga gta aca ctg cgt tcc tca	547
Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val Thr Leu Arg Ser Ser	135 140 145
ttg atc gtc ccg att atc ggc atc atg ctg ggt gcc gtg gtg tca tgc	595
Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly Ala Val Val Ser Ser	150 155 160 165
atc tcc agc ttg ttg gcc ttg caa ttg gac atg ctg cag caa ttg gga	643
Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met Leu Gln Gln Leu Gly	170 175 180
aca tgg ttt gcg ggt tcc ttg aaat aca gtg ttg cgc gga cag tac gaa	691
Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe Arg Gly Gln Tyr Glu	185 190 195
gtg ctg tgg atc gtt gtc atc gtc gtt att gca gtg ttg ttg ttg gca	739
Val Leu Trp Ile Val Val Ile Val Val Ile Ala Val Phe Phe Phe Ala	200 205 210
gac cgg ctg acc gta gct ggc ctt ggc gag gaa atc gcg aca aac gtg	787

Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu Ile Ala Thr Asn Val  
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 Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly Thr Gly Leu Ile Ala  
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 Ile Ala Thr Gly Val Val Thr Val Val Val Gly Ser Leu Pro Phe Leu  
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 Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly Ile Ala Ile Val Thr  
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 Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala Pro Phe Glu Ile Pro  
 295 300 305  
 gtt tca gta atc ctg ggc atc atc ggc gca gtg gtc ttc gtg atc atg 1075  
 Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val Val Phe Val Ile Met  
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&lt;210&gt; 202

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 202

Met Ala Thr Pro Ala Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg  
 1 5 10 15  
 Thr Arg Ala Lys Leu Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe  
 20 25 30  
 Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile  
 35 40 45  
 Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro  
 50 55 60  
 Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly  
 65 70 75 80  
 Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr  
 85 90 95  
 Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr  
 100 105 110  
 Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val  
 115 120 125

Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val  
 130 135 140  
 Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly  
 145 150 155 160  
 Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met  
 165 170 175  
 Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe  
 180 185 190  
 Arg Gly Gln Tyr Glu Val Leu Trp Ile Val Val Ile Val Val Ile Ala  
 195 200 205  
 Val Phe Phe Phe Ala Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu  
 210 215 220  
 Ile Ala Thr Asn Val Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly  
 225 230 235 240  
 Thr Gly Leu Ile Ala Ile Ala Thr Gly Val Val Thr Val Val Val Gly  
 245 250 255  
 Ser Leu Pro Phe Leu Gly Leu Ile Val Pro Asn Val Val Ser Met Phe  
 260 265 270  
 Arg Gly Asp Asp Leu Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly  
 275 280 285  
 Ile Ala Ile Val Thr Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala  
 290 295 300  
 Pro Phe Glu Ile Pro Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val  
 305 310 315 320  
 Val Phe Val Ile Met Ile Val Arg Gln Arg Gly Arg Gly  
 325 330

<210> 203  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(726)  
 <223> RXN01285

<400> 203  
 ctc aac gtc acc atc ccc gac aac acc ttc acc gcc atc atc ggc ccc 48  
 Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro  
 1 5 10 15  
 aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc 96  
 Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu  
 20 25 30  
 aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca 144



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<210> 204
<211> 242
<212> PRT
<213> Corynebacterium glutamicum
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<213> *Corynebacterium glutamicum*

&lt;400&gt; 204

Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro  
 1 5 10 15  
 Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu  
 20 25 30  
 Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser  
 35 40 45  
 Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr  
 50 55 60  
 Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly  
 65 70 75 80  
 Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu  
 85 90 95  
 Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala  
 100 105 110  
 Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp  
 115 120 125  
 Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu  
 130 135 140  
 Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu  
 145 150 155 160  
 Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His  
 165 170 175  
 Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys  
 180 185 190  
 Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala  
 195 200 205  
 Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp  
 210 215 220  
 Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala  
 225 230 235 240  
 Gly Ala

&lt;210&gt; 205

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(543)

&lt;223&gt; FRXA01285

&lt;400&gt; 205

cca cag acc tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc 48  
 Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile  
 1 5 10 15

gcg cgc ggg cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc 96  
 Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr  
 20 25 30

tcc gac gaa gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc 144  
 Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr  
 35 40 45

gaa ctt gca gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa 192  
 Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln  
 50 55 60

cga gtg tgg gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt 240  
 Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu  
 65 70 75 80

ctc gac gag ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc 288  
 Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu  
 85 90 95

ttg gaa ttg ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act 336  
 Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr  
 100 105 110

gtg ctt cac gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc 384  
 Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile  
 115 120 125

gtg atg aaa gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc 432  
 Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val  
 130 135 140

tta act gcc gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc 480  
 Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile  
 145 150 155 160

tcc cca gac ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg 528  
 Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg  
 165 170 175

tct cgc gca gga gct taagtagcta cccctccaac gga 566  
 Ser Arg Ala Gly Ala  
 180

&lt;210&gt; 206

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 206

Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile  
 1 5 10 15

Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr  
 20 25 30

Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr  
 35 40 45

Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln  
 50 55 60

Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu  
 65 70 75 80

Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu  
 85 90 95

Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr  
 100 105 110

Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile  
 115 120 125

Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val  
 130 135 140

Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile  
 145 150 155 160

Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg  
 165 170 175

Ser Arg Ala Gly Ala  
 180

<210> 207  
 <211> 936  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXA02728

<400> 207  
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tcataatggt ggcgcgaatg atgaaaaggg cgtgcactaa atg gcc att gtt tcc 115  
 Met Ala Ile Val Ser  
 1 5

ctc gac aac gtc acc gta tcc att gaa gga aaa aag ctt ctc gac gcc 163  
 Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys Lys Leu Leu Asp Ala  
 10 15 20

gtc tcc ctc aag gcc tac ccc ggg gaa gtg ttg gga ctc atc ggc cca 211  
 Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu Gly Leu Ile Gly Pro  
 25 30 35

aac ggt gcc gga aaa tcc act ctg ctg agt gtc ctt tca ggc gat cgg 259  
 Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val Leu Ser Gly Asp Arg  
 40 45 50

ctt ccc gat tca ggc gaa gtc aac gtc ggt ggc tta gat ccc gca aca 307

Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly Leu Asp Pro Ala Thr  
 55 60 65  
 gca gcg gca tcc gat atg gcc agg gtg cga gca gtc atg ctt caa gat 355  
 Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala Val Met Leu Gln Asp 85  
 70 75 80  
 gtc agc gtg gca ttt tcc ttc ctc gtg tgg gac gtc gta gaa atg ggc 403  
 Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp Val Val Glu Met Gly 100  
 90 95  
 agg cgg ccg tgg cag aag gcg tca acc ccc gaa gag gat cat gaa atc 451  
 Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu Glu Asp His Glu Ile 115  
 105 110  
 atc gaa gca gcg ctt gcc gcc acc tcg gta tcg cac ctt gcc gaa cgt 499  
 Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser His Leu Ala Glu Arg 130  
 120 125  
 gaa atc acc aca ctg tca ggc ggc gag cgg gca cgc gtt gcc ttg tcc 547  
 Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala Arg Val Ala Leu Ser 145  
 135 140  
 cgt gtc ctt gct cag caa acc ccc att gtg ctg ttg gac gaa cca aca 595  
 Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu Leu Asp Glu Pro Thr 165  
 150 155 160  
 gcc gcg atg gat atc agc cac caa gaa caa act ctg ggc aca gcg cga 643  
 Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr Leu Gly Thr Ala Arg 180  
 170 175  
 gca ctg gca gcc gcc ggg gca gca gtg att gtg gtc ctt cat gat ctc 691  
 Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val Val Leu His Asp Leu 195  
 185 190  
 aat gcg gcc gct gca tat tgc gac agc att gtg tgt ctc agt gat ggt 739  
 Asn Ala Ala Ala Tyr Cys Asp Ser Ile Val Cys Leu Ser Asp Gly 210  
 200 205  
 cga gtg att gcc tcc ggt tct gtt gat cag gtg tat tcc acg gaa acg 787  
 Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val Tyr Ser Thr Glu Thr 225  
 215 220  
 ctg tcc cgt gtt tac ggt tgg cct atc agg gtc gat cat agt gga aaa 835  
 Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val Asp His Ser Gly Lys 245  
 230 235 240  
 tat gtt cga gtg gag ccg gac cgt tct gag gcg aat tta ccc tcc gta 883  
 Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala Asn Leu Pro Ser Val 260  
 250 255  
 cta cag gtg aaa aat acg gtt tca cca gct tagatacatg actaactaag 933  
 Leu Gln Val Lys Asn Thr Val Ser Pro Ala 270  
 265  
 gtt 936

&lt;210&gt; 208

&lt;211&gt; 271

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 208

Met Ala Ile Val Ser Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys  
1 5 10 15  
Lys Leu Leu Asp Ala Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu  
20 25 30  
Gly Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val  
35 40 45  
Leu Ser Gly Asp Arg Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly  
50 55 60  
Leu Asp Pro Ala Thr Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala  
65 70 75 80  
Val Met Leu Gln Asp Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp  
85 90 95  
Val Val Glu Met Gly Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu  
100 105 110  
Glu Asp His Glu Ile Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser  
115 120 125  
His Leu Ala Glu Arg Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala  
130 135 140  
Arg Val Ala Leu Ser Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu  
145 150 155 160  
Leu Asp Glu Pro Thr Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr  
165 170 175  
Leu Gly Thr Ala Arg Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val  
180 185 190  
Val Leu His Asp Leu Asn Ala Ala Ala Ala Tyr Cys Asp Ser Ile Val  
195 200 205  
Cys Leu Ser Asp Gly Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val  
210 215 220  
Tyr Ser Thr Glu Thr Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val  
225 230 235 240  
Asp His Ser Gly Lys Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala  
245 250 255  
Asn Leu Pro Ser Val Leu Gln Val Lys Asn Thr Val Ser Pro Ala  
260 265 270

<210> 209

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<400>	209	
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cagcatgcgc aagcgcacgcg gattggggct gtaaaaaactc atg cct caa tta gtt	115	
		Met Pro Gln Leu Val 1 5
gaa att cgt gat ctg aac gtt gaa ttc ccc tct cgc cat gca gtg aaa	163	
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys		10 15 20
aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc	211	
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly		25 30 35
cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg	259	
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu		40 45 50
gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg	307	
Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser		55 60 65
aaa agc gct aaa gcc cga gcc cgc ctg ctg tca ctg gtg ccg caa aac	355	
Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn		70 75 80 85
acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc	403	
Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly		90 95 100
cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga	451	
Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg		105 110 115
cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctg gac atc gcc	499	
Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala		120 125 130
gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctg atc cac	547	
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His		135 140 145
atc ggc cga gcg ctg gcc caa gac acc gcc gtc gtg ctt ctg gac gag	595	
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu		150 155 160 165
ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctg	643	
Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu		170 175 180
ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac	691	
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His		185 190 195
gat ctg aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc	739	
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala		

200	205	210	
gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct			787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro			
215	220	225	
gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat			835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp			
230	235	240	245
ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt			880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe			
250	255	260	
tgattgaaag tttgacttaa aaa			903

<210> 210  
 <211> 260  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 210  
 Met Pro Gln Leu Val Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser  
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 Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val  
 20 25 30  
 Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser  
 35 40 45  
 Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly  
 50 55 60  
 Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser  
 65 70 75 80  
 Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp  
 85 90 95  
 Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu  
 100 105 110  
 Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn  
 115 120 125  
 Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln  
 130 135 140  
 Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val  
 145 150 155 160  
 Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val  
 165 170 175  
 Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val  
 180 185 190  
 Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His  
 195 200 205



Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg  
 210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile  
 225 230 235 240

Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His  
 245 250 255

Pro Asn Pro Phe  
 260

<210> 211  
 <211> 903  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(880)  
 <223> FRXA02864

<400> 211  
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 cagcatgctc aagcgacgag gattggggct gtaaaaactc Met Pro Gln Leu Val 115  
 1 5  
 gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163  
 Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys 20  
 10 15  
 aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211  
 Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly 35  
 25 30  
 cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259  
 Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu 50  
 40 45  
 gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg 307  
 Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser 65  
 55 60  
 aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac 355  
 Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn 85  
 70 75 80  
 acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc 403  
 Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly 100  
 90 95  
 cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga 451  
 Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg 115  
 105 110  
 cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc 499  
 Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala

120	125	130	
gag cag ccc gtc aac gaa tta tgc ggc ggc cag cag cag ctc atc cac			547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His			
135	140	145	
atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag			595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu			
150	155	160	165
ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc			643
Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu			
	170	175	180
ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac			691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His			
	185	190	195
gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc			739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala			
	200	205	210
gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct			787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro			
	215	220	225
gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat			835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp			
	230	235	240
ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt			880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe			
	250	255	260
tgattgaaag ttgacttaa aaa			903

&lt;210&gt; 212

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 212

Met	Pro	Gln	Leu	Val	Glu	Ile	Arg	Asp	Leu	Asn	Val	Glu	Phe	Pro	Ser
1				5					10					15	

Arg	His	Ala	Val	Lys	Asn	Val	Ser	Phe	Ser	Ala	Pro	Ala	Gly	Lys	Val
			20					25					30		

Thr	Ala	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Ala	Leu	Ser
		35					40					45			

Ala	Ile	Ala	Gly	Leu	Val	Glu	Ser	Thr	Gly	Glu	Val	Met	Val	Gly	Gly
		50					55				60				

Ser	Gly	Val	Ala	Ser	Lys	Ser	Ala	Lys	Ala	Arg	Ala	Arg	Leu	Leu	Ser
	65				70				75					80	

Leu	Val	Pro	Gln	Asn	Thr	Glu	Leu	Arg	Ile	Gly	Phe	Ser	Ala	Arg	Asp
				85					90					95	

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu  
 100 105 110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn  
 115 120 125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln  
 130 135 140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val  
 145 150 155 160

Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val  
 165 170 175

Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val  
 180 185 190

Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His  
 195 200 205

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg  
 210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile  
 225 230 235 240

Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His  
 245 250 255

Pro Asn Pro Phe  
 260

<210> 213  
 <211> 1149  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1126)  
 <223> RXN00523

<400> 213  
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tgtttatttg gattattcgt cgtcagaaag tcaaagagct atg agc ctt agc cat 115  
 Met Ser Leu Ser His  
 1 5

caa ctc aag cgc cag cgc gca tcg cgc aac tcc cgc agg tgg ctg att 163  
 Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser Arg Arg Trp Leu Ile  
 10 15 20

gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg 211  
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 Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln Val Leu Lys Val Leu

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gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tcg ccg Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn Gln Leu Ala Ser Pro 90 95 100			403
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ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc gcc 1075  
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<213> Corynebacterium glutamicum

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Val Leu Lys Val Leu Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser  
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Val Gly Val Leu Arg Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly  
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Leu Ala Phe Gly Ala Ala Gly Val ile Phe Gln Thr Val Leu Arg Asn  
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Gln Leu Ala Ser Pro Asp ile ile Gly ile Ser Ser Gly Ala Ser Ala  
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Ala Gly Val ile Cys ile Val Phe Phe Gly Met Ser Gln Ser Ala Val  
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Ser Ala ile Ser Leu Cys Ala Ser Leu Ala Val Ala Leu Leu ile Tyr  
 130 135 140

Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg Leu ile Leu Thr  
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Gly ile Gly ile Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu  
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Leu Ile Leu Thr Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val  
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Ser Tyr Ser Leu Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr  
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Arg Trp Leu Thr Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met  
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Pro Leu Ile Val Thr Thr Val Val Leu Ile Pro Leu Leu Val Ala Asn  
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Ala Arg Asn Val Asp Leu Met Arg Leu Gly Asn Asp Ser Ala Val Gly  
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Met Thr Ala Val Ala  
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gta gag aag cag aag gag acg tcg ata agc aaa aac ctc ggc agg cgc 163



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Lys	Val	Met	Arg	Thr	Arg	Val	Leu	Gly	Ile	Ile	Ser	Val	Thr	Leu	Leu		

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 Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile Gly Phe Val Gly Leu  
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 Met Val Pro His Val Val Arg Trp Val Val Gly Pro Asp Gln Arg Trp  
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                                     Val Val Phe Asn Ile
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aaa tct aga act gat gaa act cct gtt gct gcg tct gag ccg gtg gaa      163
Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala Ser Glu Pro Val Glu
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tcc act aga cct gtg tct gaa gct tcg aca agc cct gcg ctt aac ccc      211

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Pro	Ala	Arg	Leu	Met	Val	Val	Ser	Leu	Ile	Leu	Phe	Ala	Ile	Ala	Leu		
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 Tyr Pro Leu Ser Leu Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly  
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&lt;220&gt;

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&lt;222&gt; (1)..(582)

&lt;223&gt; RXA01822

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Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu	
65 70 75 80	
cgc ctg atg gaa atg ggt gat gat gca gct ggg gca ctt gga att tca	288
Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser	
85 90 95	
gtg gag aga aca cgg ttg ata gcc att ttg ttg gct gtg ctg ctg gtg	336
Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val	
100 105 110	
ggg atc gcc acc gca gct gca ggt ccc atc gct ttt att gca ctg gca	384
Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala	
115 120 125	
gca cct cag att gcc cgg gct ctg gcc cgg gag gat gga gtg ctg gtg	432
Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val	
130 135 140	
gct gcg tcg ata agc att ggc tct ggg ctg tta gtt gcg gcg gat tgc	480
Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys	
145 150 155 160	
cta gag caa cac gtt gat act gag ctg cac acg ccc gtt ggc ctg gtg	528
Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val	
165 170 175	
acc agt ttg ctg ggc ggg gtg tat ttg atg tgg ctt ttg agc cga aag	576
Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys	
180 185 190	
gag gca taaatgctgc aagcgcatga tct	605
Glu Ala	

&lt;210&gt; 222

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 222

Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val  
 1 5 10 15

Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met  
 20 25 30

Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala  
 35 40 45

Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile  
 50 55 60

Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu  
 65 70 75 80

Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser  
 85 90 95

Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val  
 100 105 110

Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala  
 115 120 125

Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val  
 130 135 140

Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys  
 145 150 155 160

Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val  
 165 170 175

Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys  
 180 185 190

Glu Ala

&lt;210&gt; 223

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1096)

&lt;223&gt; RXN00466

&lt;400&gt; 223

tttaaaagcg cactaagagc tcgtcaattc tttaaaacaa gctgagaatg tgaataatag 60

gatagggttaa cctgattcga ttagaaaaag gagatttgct gtg caa tcc cgc ctg 115  
 Val Gln Ser Arg Leu  
 1 5

tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163  
 Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu



	10	15	20	
tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca				211
Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr	25	30	35	
tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga				259
Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly	40	45	50	
acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt				307
Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val Val Thr Leu Gly Val	55	60	65	
acc gac gcc gat att gtc ctc gca ttg ggg acc gtc cca gta ggc aac				355
Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr Val Pro Val Gly Asn	70	75	80 85	
acc gga tac aaa ttc ttc gaa aac gga ttg gga ccg tgg act gat gag				403
Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly Pro Trp Thr Asp Glu	90	95	100	
tta gtg gaa ggc aaa gaa tta aca ctg ctt gac tct gat tcc aca cca				451
Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp Ser Asp Ser Thr Pro	105	110	115	
gat ctt gaa caa gta gca gcc ctg gag cca gac ctg att att gga gtc				499
Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp Leu Ile Ile Gly Val	120	125	130	
tct gcg ggg ttt gac gac gtt gta tac gag caa cta tct gat atc gca				547
Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln Leu Ser Asp Ile Ala	135	140	145	
ccg gtg gtc gcc cgt cca gcg gga aca gct gca tac gca gta gct cgc				595
Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala Tyr Ala Val Ala Arg	150	155	160 165	
gag gaa gct acc aac ctt gtt gcc cgt gcg atg ggg caa tca gaa aaa				643
Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met Gly Gln Ser Glu Lys	170	175	180	
gga caa gag ctc aat gag gaa aca gat gct ctg atc caa gct gcg cgt				691
Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu Ile Gln Ala Ala Arg	185	190	195	
gat gaa aat cct tct ttt gac ggt aaa aca gga acc gtc atc ttg cca				739
Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly Thr Val Ile Leu Pro	200	205	210	
tac cag ggt aaa tac ggt gcc tac ctg cca ggc gat gca cgg gga caa				787
Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly Asp Ala Arg Gly Gln	215	220	225	
ttc ctc gat tca ctt ggc att tcg ctg ccg gaa gca gtt ctt tcg cga				835
Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu Ala Val Leu Ser Arg	230	235	240 245	
gac acc ggc gac agc ttc ttt gtc gat gtc ccc gct gaa agc gtc aaa				883
Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro Ala Glu Ser Val Lys	250	255	260	

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<400> 224
Val Gln Ser Arg Leu Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val
  1                               5                      10              15
Ala Val Leu Ala Leu Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr
      20                                25                    30
Asp Ala Asp Ser Thr Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile
     35                                40                    45
Glu His Glu Phe Gly Thr Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val
    50                                55                    60
Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr
   65                                70                    75                80
Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly
      85                                90                    95
Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp
    100                             105                  110
Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp
   115                             120                  125
Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln
   130                             135                  140
Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala
  145                             150                  155                160
Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met
      165                             170                  175
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Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu  
 180 185 190  
 Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly  
 195 200 205  
 Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly  
 210 215 220  
 Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu  
 225 230 235 240  
 Ala Val Leu Ser Arg Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro  
 245 250 255  
 Ala Glu Ser Val Lys Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser  
 260 265 270  
 Asn Asp Glu Asn Leu Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr  
 275 280 285  
 Leu Asn Val Val Gln Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu  
 290 295 300  
 Arg Gly Ala Ile Thr Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu  
 305 310 315 320  
 Glu His Leu Ala Pro Arg Ile Ala Glu Ala Leu Lys  
 325 330

&lt;210&gt; 225

&lt;211&gt; 1087

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1087)

&lt;223&gt; FRXA00466

&lt;400&gt; 225

tttaaaagcg cactaagagc tcgtcaattc tttaaaacaa gctgagaatg tgaataatag 60

 gatagggttaa cctgattcga ttagaaaacg gagatttgtc gtg caa tcc cgc ctg 115  
 Val Gln Ser Arg Leu  
 1 5

 tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163  
 Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu  
 10 15 20

 tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca 211  
 Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr  
 25 30 35

 tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga 259  
 Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly  
 40 45 50

acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt 307

Thr	Thr	Thr	Ile	Asp	Asp	Val	Pro	Glu	Arg	Val	Val	Thr	Leu	Gly	Val		
55						60					65						
acc	gac	gcc	gat	att	gtc	ctc	gca	ttg	ggg	acc	gtc	cca	gta	ggc	aac	355	
Thr	Asp	Ala	Asp	Ile	Val	Leu	Ala	Leu	Gly	Thr	Val	Pro	Val	Gly	Asn		
70					75				80						85		
acc	gga	tac	aaa	ttc	ttc	gaa	aac	gga	ttg	gga	ccg	tgg	act	gat	gag	403	
Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly	Pro	Trp	Thr	Asp	Glu		
				90					95						100		
tta	gtg	gaa	ggc	aaa	gaa	tta	aca	ctg	ctt	gac	tct	gat	tcc	aca	cca	451	
Leu	Val	Glu	Gly	Lys	Glu	Leu	Thr	Leu	Leu	Asp	Ser	Asp	Ser	Thr	Pro		
			105					110						115			
gat	ctt	gaa	caa	gta	gca	gcc	ctg	gag	cca	gac	ctg	att	att	gga	gtc	499	
Asp	Leu	Glu	Gln	Val	Ala	Ala	Leu	Glu	Pro	Asp	Leu	Ile	Ile	Gly	Val		
		120					125						130				
tct	gcg	ggg	ttt	gac	gac	gtt	gta	tac	gag	caa	cta	tct	gat	atc	gca	547	
Ser	Ala	Gly	Phe	Asp	Asp	Val	Val	Tyr	Glu	Gln	Leu	Ser	Asp	Ile	Ala		
	135					140					145						
ccg	gtg	gtc	gcc	cgt	cca	gcg	gga	aca	gct	gca	tac	gca	gta	gct	cgc	595	
Pro	Val	Val	Ala	Arg	Pro	Ala	Gly	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Arg		
150					155				160						165		
gag	gaa	gct	acc	aac	ctt	gtt	gcc	cgt	gcg	atg	ggg	caa	tca	gaa	aaa	643	
Glu	Glu	Ala	Thr	Asn	Leu	Val	Ala	Arg	Ala	Met	Gly	Gln	Ser	Glu	Lys		
				170				175						180			
gga	caa	gag	ctc	aat	gag	gaa	aca	gat	gct	ctg	atc	caa	gct	gcg	cgt	691	
Gly	Gln	Glu	Leu	Asn	Glu	Glu	Thr	Asp	Ala	Leu	Ile	Gln	Ala	Ala	Arg		
			185					190					195				
gat	gaa	aat	cct	tct	ttt	gac	ggt	aaa	aca	gga	acc	gtc	atc	ttg	cca	739	
Asp	Glu	Asn	Pro	Ser	Phe	Asp	Gly	Lys	Thr	Gly	Thr	Val	Ile	Leu	Pro		
		200					205						210				
tac	cag	ggt	aaa	tac	ggt	gcc	tac	ctg	cca	ggc	gat	gca	cgg	gga	caa	787	
Tyr	Gln	Gly	Lys	Tyr	Gly	Ala	Tyr	Leu	Pro	Gly	Asp	Ala	Arg	Gly	Gln		
	215					220					225						
ttc	ctc	gat	tca	ctt	ggc	att	tcg	ctg	ccg	gaa	gca	gtt	ctt	tcg	cga	835	
Phe	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Leu	Pro	Glu	Ala	Val	Leu	Ser	Arg		
230					235					240					245		
gac	acc	ggc	gac	agc	ttc	ttt	gtc	gat	gtc	ccc	gct	gaa	agc	gtc	aaa	883	
Asp	Thr	Gly	Asp	Ser	Phe	Phe	Val	Asp	Val	Pro	Ala	Glu	Ser	Val	Lys		
				250				255						260			
gac	gta	gac	ggt	gat	gtt	ctc	ctc	gtg	ctt	tcc	aac	gac	gaa	aat	ctg	931	
Asp	Val	Asp	Gly	Asp	Val	Leu	Leu	Val	Leu	Ser	Asn	Asp	Glu	Asn	Leu		
			265					270					275				
gat	atc	aca	gca	gag	aat	cca	ctg	ttt	gaa	aca	ctc	aac	gtt	gtg	caa	979	
Asp	Ile	Thr	Ala	Glu	Asn	Pro	Leu	Phe	Glu	Thr	Leu	Asn	Val	Val	Gln		
		280					285					290					
aaa	gac	gca	gta	att	gtg	gca	aca	acc	gaa	gaa	cgc	ggg	gcg	att	acc	1027	
Lys	Asp	Ala	Val	Ile	Val	Ala	Thr	Thr	Glu	Glu	Arg	Gly	Ala	Ile	Thr		

295

300

305

tac aac tca gtg ctg tct gtt cct ttt gcg ttg gaa cat ctc gca cca 1075  
 Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu Glu His Leu Ala Pro  
 310 315 320 325

cgt att gct gag 1087  
 Arg Ile Ala Glu

&lt;210&gt; 226

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 226

Val Gln Ser Arg Leu Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val  
 1 5 10 15

Ala Val Leu Ala Leu Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr  
 20 25 30

Asp Ala Asp Ser Thr Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile  
 35 40 45

Glu His Glu Phe Gly Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val  
 50 55 60

Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr  
 65 70 75 80

Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly  
 85 90 95

Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp  
 100 105 110

Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp  
 115 120 125

Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln  
 130 135 140

Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala  
 145 150 155 160

Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met  
 165 170 175

Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu  
 180 185 190

Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly  
 195 200 205

Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly  
 210 215 220

Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu  
 225 230 235 240

<400> 227																
acggactgcc	cattgcggtg	cgcgatgac	ccgaaaccag	ctcacttcgc	gtgatccgc	60										
atccaaatcc cttttgattg aaagtttgac ttaaaaaccc							atg	aaa	aaa	tca	ctc	115				
							Met	Lys	Lys	Ser	Leu					
							1				5					
atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat	163															
Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp																
10 15 20																
tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att	211															
Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile																
25 30 35																
aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca	259															
Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr																
40 45 50																
ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc	307															
Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala																
55 60 65																
gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc	355															
Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala																
70 75 80 85																
gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc	403															
Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr																
90 95 100																

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agg 451  
 Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Arg  
                   105                                  110                                  115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499  
 Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val  
                   120                                  125                                  130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547  
 Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly  
                   135                                  140                                  145

ctc aac gtc ccg tagttaactt cgattcagac gct 582  
 Leu Asn Val Pro  
 150

<210> 228

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser  
           1                                  5                                  10                                  15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val  
                                   20                                  25                                  30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe  
           35                                  40                                  45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys  
           50                                  55                                  60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu  
           65                                  70                                  75                                  80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr  
                                   85                                  90                                  95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val  
                   100                                  105                                  110

Lys Asn Gly Gly Arg Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro  
           115                                  120                                  125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile  
           130                                  135                                  140

Asp Ile Leu Glu Gly Leu Asn Val Pro  
 145                                  150

<210> 229

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

&lt;222&gt; (101)..(1075)

&lt;223&gt; FRXA02863

&lt;400&gt; 229

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atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115  
 Met Lys Lys Ser Leu  
 1 5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163  
 Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp  
 10 15 20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att 211  
 Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile  
 25 30 35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca 259  
 Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr  
 40 45 50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc 307  
 Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala  
 55 60 65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc 355  
 Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala  
 70 75 80 85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc 403  
 Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr  
 90 95 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agc 451  
 Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Ser  
 105 110 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499  
 Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val  
 120 125 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547  
 Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly  
 135 140 145

ctc aac gtc ccc gta gtt aac ttc gat tca gac gct tgg gga gac atc 595  
 Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp Ala Trp Gly Asp Ile  
 150 155 160 165

gac gcc atc acc aaa cac cta gaa att gtg ggt gaa ctc gtc ggc gaa 643  
 Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly Glu Leu Val Gly Glu  
 170 175 180

gaa gac aaa gcc gca gaa gca atc gca gaa atc gat gca aac cgc atc 691  
 Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile Asp Ala Asn Arg Ile  
 185 190 195

gac atc gac aag cct gcc acc tcc ccc act gtg ctc act ttg atg caa 739  
 Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val Leu Thr Leu Met Gln  
 200 205 210



cgc gga cca cgc caa atg gtc atg cca gaa tct gcc atg ctc aac ggc 787  
 Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser Ala Met Leu Asn Gly  
 215 220 225  
  
 ctg atc cgc gaa gcc ggc ggc act cca gtg gta gat tct ctc ggc gcg 835  
 Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val Asp Ser Leu Gly Ala  
 230 235 240 245  
  
 gta ggc acc atc act gca gac cca gaa caa gtt gtt gcg atg gca cct 883  
 Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val Val Ala Met Ala Pro  
 250 255 260  
  
 gag atc atc atc att cag gac ttc caa ggt aaa ggc cga gag aac ttc 931  
 Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe  
 265 270 275  
  
 gct aat ttc ctc tcc aac cca gcg cta gcc aac gtt ccc gcc att gaa 979  
 Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu  
 280 285 290  
  
 aac gac aag att ttc tac gcc gac act gtc acc act gga gtt act gca 1027  
 Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala  
 295 300 305  
  
 ggt acc gat atc acc act ggt ctg cag caa gtg gca gaa atg ctg agc 1075  
 Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser  
 310 315 320 325  
  
 tagttttgag atgttgaaac tag 1098

&lt;210&gt; 230

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 230

Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser  
1 5 10 15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val  
20 25 30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe  
35 40 45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys  
50 55 60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu  
65 70 75 80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr  
85 90 95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val  
100 105 110

Lys Asn Gly Gly Ser Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro  
115 120 125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile  
 130 135 140  
 Asp Ile Leu Glu Gly Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp  
 145 150 155 160  
 Ala Trp Gly Asp Ile Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly  
 165 170 175  
 Glu Leu Val Gly Glu Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile  
 180 185 190  
 Asp Ala Asn Arg Ile Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val  
 195 200 205  
 Leu Thr Leu Met Gln Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser  
 210 215 220  
 Ala Met Leu Asn Gly Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val  
 225 230 235 240  
 Asp Ser Leu Gly Ala Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val  
 245 250 255  
 Val Ala Met Ala Pro Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys  
 260 265 270  
 Gly Arg Glu Asn Phe Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn  
 275 280 285  
 Val Pro Ala Ile Glu Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr  
 290 295 300  
 Thr Gly Val Thr Ala Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val  
 305 310 315 320  
 Ala Glu Met Leu Ser  
 325

<210> 231  
 <211> 776  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(775)  
 <223> RXS03221

<400> 231  
 caaaagtatt caaaaaaagt ttgttatgta cgattgacgg gacatatcgt gtctgccacg 60  
 attaaagaca ttggtgatgt gaatcactgc ctactacatc gtg ttt cgt gac cct 115  
 Val Phe Arg Asp Pro  
 1 5  
 gca cct cca agt aag ggc acg aca aac tta gga gac aag atg gct agt 163  
 Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly Asp Lys Met Ala Ser  
 10 15 20

acc ttc att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca 211  
 Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro  
 25 30 35

ctc aca gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt 259  
 Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val  
 40 45 50

gcg acg ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac 307  
 Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn  
 55 60 65

ggt gca ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc 355  
 Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr  
 70 75 80 85

gag ggt gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg 403  
 Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala  
 90 95 100

atg ttt ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc 451  
 Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile  
 105 110 115

atc tca ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt 499  
 Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe  
 120 125 130

gct cca tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc 547  
 Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu  
 135 140 145

gca gtt ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt 595  
 Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu  
 150 155 160 165

gct cct ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg 643  
 Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met  
 170 175 180

att gtt gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga 691  
 Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly  
 185 190 195

aat gtt ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att 739  
 Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile  
 200 205 210

gcc gca atc cca gca att gcc ctc ttc ttt gga atg c 776  
 Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly Met  
 215 220 225

&lt;210&gt; 232

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 232

Val Phe Arg Asp Pro Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly

1	5	10	15
Asp Lys Met	Ala Ser Thr Phe Ile	Gln Ala Asp Ser Pro	Glu Lys Ser
	20	25	30
Lys Lys Leu	Pro Pro Leu Thr	Glu Gly Pro Tyr Arg	Lys Arg Leu Phe
	35	40	45
Tyr Val Ala	Leu Val Ala Thr	Phe Gly Gly Leu Leu	Phe Gly Tyr Asp
	50	55	60
Thr Gly Val	Ile Asn Gly Ala	Leu Asn Pro Met Thr	Arg Glu Leu Gly
	65	70	75
Leu Thr Ala	Phe Thr Glu Gly	Val Val Thr Ser	Ser Leu Leu Phe Gly
	85	90	95
Ala Ala Ala	Gly Ala Met Phe	Phe Gly Arg Ile Ser	Asp Asn Trp Gly
	100	105	110
Arg Arg Lys	Thr Ile Ile Ser	Leu Ala Val Ala	Phe Phe Val Gly Thr
	115	120	125
Met Ile Cys	Val Phe Ala Pro	Ser Phe Ala Val	Met Val Val Gly Arg
	130	135	140
Val Leu Leu	Gly Leu Ala Val	Gly Gly Ala Ser	Thr Val Val Pro Val
	145	150	155
Tyr Leu Ala	Glu Leu Ala Pro	Phe Glu Ile Arg	Gly Ser Leu Ala Gly
	165	170	175
Arg Asn Glu	Leu Met Ile Val	Val Gly Gln Leu	Ala Ala Phe Val Ile
	180	185	190
Asn Ala Ile	Ile Gly Asn Val	Phe Gly His His	Asp Gly Val Trp Arg
	195	200	205
Tyr Met Leu	Ala Ile Ala Ala	Ile Pro Ala Ile	Ala Leu Phe Phe Gly
	210	215	220
Met			
225			

<210> 233  
 <211> 718  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(718)  
 <223> FRXA01986

<400> 233  
 gccacgatta aagacattgg tgatgtgaat cactgcctac tacatcgtgt ttcgtgaccc 60  
 tgcacctcca agtaagggca cgacaaactt aggagacaag atg gct agt acc ttc 115  
 Met Ala Ser Thr Phe  
 1 5

att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca ctc aca 163  
 Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro Leu Thr  
 10 15 20

gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt gcg acg 211  
 Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val Ala Thr  
 25 30 35

ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac ggt gca 259  
 Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn Gly Ala  
 40 45 50

ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc gag ggt 307  
 Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr Glu Gly  
 55 60 65

gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg atg ttt 355  
 Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala Met Phe  
 70 75 80 85

ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc atc tca 403  
 Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile Ile Ser  
 90 95 100

ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt gct cca 451  
 Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe Ala Pro  
 105 110 115

tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc gca gtt 499  
 Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu Ala Val  
 120 125 130

ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt gct cct 547  
 Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro  
 135 140 145

ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg att gtt 595  
 Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met Ile Val  
 150 155 160 165

gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga aat gtt 643  
 Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly Asn Val  
 170 175 180

ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att gcc gca 691  
 Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile Ala Ala  
 185 190 195

atc cca gca att gcc ctc ttc ttt gga 718  
 Ile Pro Ala Ile Ala Leu Phe Phe Gly  
 200 205

&lt;210&gt; 234

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys

1	5	10	15
Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val	20	25	30
Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly	35	40	45
Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr	50	55	60
Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala	65	70	75
Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg	85	90	95
Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile	100	105	110
Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu	115	120	125
Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu	130	135	140
Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn	145	150	155
Glu Leu Met Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala	165	170	175
Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met	180	185	190
Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly	195	200	205

&lt;210&gt; 235

&lt;211&gt; 1118

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1095)

&lt;223&gt; RXN02447

&lt;400&gt; 235

aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc	48
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg	
1 5 10 15	
ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg	96
Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu	
20 25 30	
ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt	144
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val	
35 40 45	

att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala 50 55 60	192
gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp 65 70 75 80	240
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr 85 90 95	288
gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala 100 105 110	336
gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser 115 120 125	384
ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile 130 135 140	432
ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly 145 150 155 160	480
atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met 165 170 175	528
tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg Tyr Tyr Gly Thr Arg Val Leu Glu Ser Gly Met Ser Ala Glu Met 180 185 190	576
gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly 195 200 205	624
ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe 210 215 220	672
atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg atc gca gct Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala 225 230 235 240	720
gcc ggc act ctc ctt cca gaa ggt aac tcc att cga cca ttc gcc atc Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile 245 250 255	768
atg atc ctt gtt gtt ggg ttc gtg ctc tcc atg cag act ttc ctc aac Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn 260 265 270	816
gtt gca gtg tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys 275 280 285	864

ggt atc ggc acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc 912  
 Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly  
 290 295 300  
  
 gtc cta gcg ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc 960  
 Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr  
 305 310 315 320  
  
 ttc tcc ttc ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc 1008  
 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe  
 325 330 335  
  
 gtc acc aag ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc 1056  
 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu  
 340 345 350  
  
 gat cac gca gca ttc acc ggc cag atc ttc aag aag gct taaaccccct 1105  
 Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala  
 355 360 365  
  
 ccgatctctt tgg 1118

&lt;210&gt; 236

&lt;211&gt; 365

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 236

Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg  
 1 5 10 15  
  
 Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu  
 20 25 30  
  
 Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val  
 35 40 45  
  
 Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala  
 50 55 60  
  
 Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp  
 65 70 75 80  
  
 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr  
 85 90 95  
  
 Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala  
 100 105 110  
  
 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser  
 115 120 125  
  
 Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile  
 130 135 140  
  
 Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly  
 145 150 155 160  
  
 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met  
 165 170 175



Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met  
 180 185 190  
 Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly  
 195 200 205  
 Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe  
 210 215 220  
 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala  
 225 230 235 240  
 Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile  
 245 250 255  
 Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn  
 260 265 270  
 Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys  
 275 280 285  
 Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly  
 290 295 300  
 Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr  
 305 310 315 320  
 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe  
 325 330 335  
 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu  
 340 345 350  
 Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala  
 355 360 365

&lt;210&gt; 237

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(270)

&lt;223&gt; FRXA02447

&lt;400&gt; 237

tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag ggt atc ggc 48  
 Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly  
 1 5 10 15

acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc gtc cta gcg 96  
 Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala  
 20 25 30

ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc ttc tcc ttc 144  
 Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe  
 35 40 45

ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc gtc acc aag 192  
 Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys  
     50                    55                    60

ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc gat cac gca 240  
 Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala  
     65                    70                    75                    80

gca ttc acc ggc cag atc ttc aag aag gct taaacccccct ccgatctctt 290  
 Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala  
                     85                    90

tgg 293

<210> 238

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly  
     1                    5                    10                    15

Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala  
             20                    25                    30

Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe  
             35                    40                    45

Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys  
     50                    55                    60

Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala  
     65                    70                    75                    80

Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala  
                     85                    90

<210> 239

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(711)

<223> FRXA02769

<400> 239

aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc 48  
 Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg  
     1                    5                    10                    15

ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg 96  
 Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu  
             20                    25                    30

ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt 144  
 Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val

35	40	45	
att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala 50 55 60			192
gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp 65 70 75 80			240
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr 85 90 95			288
gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala 100 105 110			336
gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser 115 120 125			384
ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile 130 135 140			432
ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly 145 150 155 160			480
atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met 165 170 175			528
tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met 180 185 190			576
gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly 195 200 205			624
ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe 210 215 220			672
atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu 225 230 235			711

&lt;210&gt; 240

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 240

Thr	Val	Val	Pro	Val	Tyr	Leu	Ala	Glu	Leu	Ala	Pro	Leu	Glu	Ile	Arg
1				5					10					15	

Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu

20	25	30
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val 35 40 45		
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala 50 55 60		
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp 65 70 75 80		
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr 85 90 95		
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala 100 105 110		
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser 115 120 125		
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile 130 135 140		
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly 145 150 155 160		
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met 165 170 175		
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met 180 185 190		
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly 195 200 205		
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe 210 215 220		
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu 225 230 235		

<210> 241  
 <211> 725  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (3)..(695)  
 <223> RXS03220

<400> 241

cc atg ggc tta agg gaa att ttg tcc agc aag tgg ctt gtg cgc atc ctc 50  
 Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu  
 1 5 10 15

ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac 98  
 Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn  
 20 25 30

<400> 242  
Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu  
1 5 10 15

Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn  
                   20                                  25                                  30  
 Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser  
                   35                                  40                                  45  
 Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val  
                   50                                  55                                  60  
 Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg  
                   65                                  70                                  75                                  80  
 Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu  
                                   85                                  90                                  95  
 Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro  
                                   100                                  105                                  110  
 Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr  
                   115                                  120                                  125  
 Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu  
                   130                                  135                                  140  
 Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile  
                   145                                  150                                  155                                  160  
 Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val  
                                   165                                  170                                  175  
 Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala  
                   180                                  185                                  190  
 Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu  
                   195                                  200                                  205  
 Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp  
                   210                                  215                                  220  
 Ile Arg Lys Gly Lys Val His  
                   225                                  230

&lt;210&gt; 243

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA02762

&lt;400&gt; 243

ttcccagtcg gcgacacctc tcgccccctac gttatcttga ctctggttgt ggtcttcgtg 60

ggatccatgc agaccttcct caacggtagc tacctggggtt atg ctc tct gag ctc 115

Met Leu Ser Glu Leu

1

5

ttc ccg ctg gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc 163  
 Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe  
                   10                  15                  20

ctc tgg atc gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg 211  
 Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met  
                   25                  30                  35

gaa gca gta gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt 259  
 Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly  
                   40                  45                  50

gtg gtt gcc ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga 307  
 Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly  
                   55                  60                  65

cgt acc ttg gag gag att gat gag gat gtt act tcc ggt gtc att ttc 355  
 Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe  
                   70                  75                  80                  85

aac aag gac atc cga aaa gga aag gtg cac taaaaaccca gacactgcat 405  
 Asn Lys Asp Ile Arg Lys Gly Lys Val His  
                   90                  95

aga 408

<210> 244

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Leu Ser Glu Leu Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly  
                   1                  5                  10                  15

Ile Ser Val Phe Phe Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe  
                   20                  25                  30

Phe Pro Thr Ile Met Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met  
                   35                  40                  45

Phe Ala Gly Ile Gly Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val  
                   50                  55                  60

Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr  
                   65                  70                  75                  80

Ser Gly Val Ile Phe Asn Lys Asp Ile Arg Lys Gly Lys Val His  
                   85                  90                  95

<210> 245

<211> 324

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> FRXA02761

&lt;400&gt; 245

cagggtgttc tcattgaggt gggtttctccg agaatgcagc tttgatcgcc aacgtggcgc 60

cagaagtgat cgcagttgtc gggcattcat cgcactgtgg atg atg gat ggt atc 115  
Met Met Asp Gly Ile  
1 5

aac cgc cgt acc acc ctc att acc ggt tat tct ctc acc acc att agc 163  
Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser  
10 15 20

cac gta ttg atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct 211  
His Val Leu Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro  
25 30 35

ctt cgc ccc tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc 259  
Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser  
40 45 50

atg cag acc ttc ctc aac ggt agc tac ctg ggt tat gct ctc 301  
Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly Tyr Ala Leu  
55 60 65

tgagctcttc ccgctggcaa tgc 324

&lt;210&gt; 246

&lt;211&gt; 67

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 246

Met Met Asp Gly Ile Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser  
1 5 10 15

Leu Thr Thr Ile Ser His Val Leu Ile Gly Ile Ala Ser Val Ala Phe  
20 25 30

Pro Val Gly Asp Pro Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val  
35 40 45

Val Phe Val Gly Ser Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly  
50 55 60

Tyr Ala Leu  
65

&lt;210&gt; 247

&lt;211&gt; 1242

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1219)

&lt;223&gt; RXA00123

&lt;400&gt; 247

gaaggatcgt cagaatagct ctggaatagg ccatttctta cttcatcggc aatactgact 60



tagtagaaat tgctgtccag aactgttgaa ggagttgaaa atg cca aag aat tac	115
Met Pro Lys Asn Tyr	
1 5	
gac atc aac ggg gcg atc cgc aga cgg gat atg ctc aga cgt cgg tac	163
Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met Leu Arg Arg Arg Tyr	
10 15 20	
ctt cct gat tcg gca aat tca act cct gta cct gaa gag gtt tct ccg	211
Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro Glu Glu Val Ser Pro	
25 30 35	
ctg acc cgc tat gtc acc gac ggc atc ccg aag cgc cca ccg ctg ggt	259
Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys Arg Pro Pro Leu Gly	
40 45 50	
gcc act gtt gct gac ggt tta aaa ttc gcc gaa ggc gcc tcc aac cgc	307
Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu Gly Ala Ser Asn Arg	
55 60 65	
atg gtc atg tcg ctg tac cct gcg cca tcc aag ccc gca atc gag gaa	355
Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys Pro Ala Ile Glu Glu	
70 75 80 85	
ttg gca gag gcc tgg gac ctc cac ccc acc atc gta gaa gac ttg ctc	403
Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile Val Glu Asp Leu Leu	
90 95 100	
ctt ggt cag cag cgc cca aaa cta gac cgc tac gaa gac atc att ttt	451
Leu Gly Gln Gln Arg Pro Lys Leu Asp Arg Tyr Glu Asp Ile Ile Phe	
105 110 115	
atc gcg atc cgc tcc gcg cgc tac atc gac tcc cgc gaa gag gtg gac	499
Ile Ala Ile Arg Ser Ala Arg Tyr Ile Asp Ser Arg Glu Glu Val Asp	
120 125 130	
ttc tcc gaa ttc cac atc ctc atg aag cct cag gcc ata gcc att ttg	547
Phe Ser Glu Phe His Ile Leu Met Lys Pro Gln Ala Ile Ala Ile Leu	
135 140 145	
tgc cag gat aac caa tgg att gac ggc acc agc gcc gcc agc ttc agc	595
Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser Ala Ala Ser Phe Ser	
150 155 160 165	
aac ccc gag gag atc gat aag cgc ata aaa aca ttg ctt gcc gac gcc	643
Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr Leu Leu Ala Asp Ala	
170 175 180	
gag tta ctc tcg tcc ggc ccc cgc gcc gcg gcc tat agg ctt ctc gac	691
Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala Tyr Arg Leu Leu Asp	
185 190 195	
gcc atc gtc gac ggc ttc tcc ccc gtt ctt aga ggc atc gcc atc gac	739
Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg Gly Ile Ala Ile Asp	
200 205 210	
cag gaa cag att gag cgc cag gtg ttc tcc ggc gac gcc gcc gtc gcc	787
Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly Asp Ala Ala Val Ala	
215 220 225	

gaa cgt att tac aac ctg tcc caa gaa atc atc gac atg cag cac acc 835  
 Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile Asp Met Gln His Thr  
 230 235 240 245  
  
 acc agc tca gtt acc gaa gtg gtg caa cgc ctc aac aaa gac ttc atc 883  
 Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu Asn Lys Asp Phe Ile  
 250 255 260  
  
 cga agt ggc atg tcc gaa gaa ctc cgc gcc tac ctc gac gac gtc gcc 931  
 Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr Leu Asp Asp Val Ala  
 265 270 275  
  
 gac cac ctc acc cgc gac aac acc cgc gtc tcc gaa tac cgc gaa tcc 979  
 Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser Glu Tyr Arg Glu Ser  
 280 285 290  
  
 cta tcc caa att ttg aac gtc aac gcc acc ctt gta gcc caa cgc caa 1027  
 Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu Val Ala Gln Arg Gln  
 295 300 305  
  
 aac gaa gac atg aag aaa atc tcc gga tgg gcc gcc atc atc ttc gcc 1075  
 Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala Ala Ile Ile Phe Ala  
 310 315 320 325  
  
 cca acc ctc gtg tcc tcc atc tac ggc atg aac ttc gac atc atg cca 1123  
 Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn Phe Asp Ile Met Pro  
 330 335 340  
  
 gaa ctt cac tgg gcg ttt ggc tac ccg ttg gct ctc tta gca atg ctc 1171  
 Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala Leu Leu Ala Met Leu  
 345 350 355  
  
 gga ttc acc ctc ctt ttg tac tgg atc ttc aaa cgc agt aag tgg atg 1219  
 Gly Phe Thr Leu Leu Leu Tyr Trp Ile Phe Lys Arg Ser Lys Trp Met  
 360 365 370  
  
 tgagacaaaa accgaaaaac caa 1242

&lt;210&gt; 248

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 248

Met Pro Lys Asn Tyr Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met  
 1 5 10 15  
  
 Leu Arg Arg Arg Tyr Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro  
 20 25 30  
  
 Glu Glu Val Ser Pro Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys  
 35 40 45  
  
 Arg Pro Pro Leu Gly Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu  
 50 55 60  
  
 Gly Ala Ser Asn Arg Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys  
 65 70 75 80  
  
 Pro Ala Ile Glu Glu Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile

85					90					95					
Val	Glu	Asp	Leu	Leu	Leu	Gly	Gln	Gln	Arg	Pro	Lys	Leu	Asp	Arg	Tyr
			100					105					110		
Glu	Asp	Ile	Ile	Phe	Ile	Ala	Ile	Arg	Ser	Ala	Arg	Tyr	Ile	Asp	Ser
		115					120					125			
Arg	Glu	Glu	Val	Asp	Phe	Ser	Glu	Phe	His	Ile	Leu	Met	Lys	Pro	Gln
	130					135					140				
Ala	Ile	Ala	Ile	Leu	Cys	Gln	Asp	Asn	Gln	Trp	Ile	Asp	Gly	Thr	Ser
145					150					155					160
Ala	Ala	Ser	Phe	Ser	Asn	Pro	Glu	Glu	Ile	Asp	Lys	Arg	Ile	Lys	Thr
				165					170					175	
Leu	Leu	Ala	Asp	Ala	Glu	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ala	Ala	Ala
			180					185					190		
Tyr	Arg	Leu	Leu	Asp	Ala	Ile	Val	Asp	Gly	Phe	Ser	Pro	Val	Leu	Arg
		195					200					205			
Gly	Ile	Ala	Ile	Asp	Gln	Glu	Gln	Ile	Glu	Arg	Gln	Val	Phe	Ser	Gly
	210					215					220				
Asp	Ala	Ala	Val	Ala	Glu	Arg	Ile	Tyr	Asn	Leu	Ser	Gln	Glu	Ile	Ile
225					230					235					240
Asp	Met	Gln	His	Thr	Thr	Ser	Ser	Val	Thr	Glu	Val	Val	Gln	Arg	Leu
			245						250					255	
Asn	Lys	Asp	Phe	Ile	Arg	Ser	Gly	Met	Ser	Glu	Glu	Leu	Arg	Ala	Tyr
			260					265					270		
Leu	Asp	Asp	Val	Ala	Asp	His	Leu	Thr	Arg	Asp	Asn	Thr	Arg	Val	Ser
		275					280					285			
Glu	Tyr	Arg	Glu	Ser	Leu	Ser	Gln	Ile	Leu	Asn	Val	Asn	Ala	Thr	Leu
	290					295					300				
Val	Ala	Gln	Arg	Gln	Asn	Glu	Asp	Met	Lys	Lys	Ile	Ser	Gly	Trp	Ala
305					310					315					320
Ala	Ile	Ile	Phe	Ala	Pro	Thr	Leu	Val	Ser	Ser	Ile	Tyr	Gly	Met	Asn
				325					330					335	
Phe	Asp	Ile	Met	Pro	Glu	Leu	His	Trp	Ala	Phe	Gly	Tyr	Pro	Leu	Ala
			340					345					350		
Leu	Leu	Ala	Met	Leu	Gly	Phe	Thr	Leu	Leu	Leu	Tyr	Trp	Ile	Phe	Lys
		355					360					365			
Arg	Ser	Lys	Trp	Met											
			370												

&lt;210&gt; 249

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; RXA02441

&lt;400&gt; 249

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ccggcgacca gggcgcgggga gatgaatgaa acgtcaaaag gcactatgag ggcgtcagta 60

aaaaacttca tttgaaaatg ataaccgtta tcattaagga atg gca gaa ctc agc 115
                                         Met Ala Glu Leu Ser
                                         1 5

gtc cgg aat ctc aca tgc aca tac ggc aat cac atc gcg ctc aac aac 163
Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His Ile Ala Leu Asn Asn
                        10 15 20

atc acg gca cgc ttc cca acc gga aaa ata act gcc ctc atc ggc agc 211
Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr Ala Leu Ile Gly Ser
                        25 30 35

aac ggc tcc gga aaa tcc aca ctg ttg gaa act ttg gcg ggc atg ctg 259
Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr Leu Ala Gly Met Leu
                        40 45 50

gca ccc cgc agc gga agc att aac aac ctt gtg cca gaa atc gcg ttc 307
Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val Pro Glu Ile Ala Phe
                        55 60 65

gtc ccc caa cgc agc cac gtc tcc cat aat ttg ccc atc acg atc aga 355
Val Pro Gln Arg Ser His Val Ser His Asn Leu Pro Ile Thr Ile Arg
                        70 75 80 85

caa aca gtc agc atg ggg cga tgg tca gcc aag aaa aac tgg caa cga 403
Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys Lys Asn Trp Gln Arg
                        90 95 100

ctc act gcc gca gat tgc aac atc gtg gac agc tgc ctc gac cgg ctc 451
Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser Cys Leu Asp Arg Leu
                        105 110 115

gaa atc tcc ggc ctc gcc gac cgc ccc ctc ggc gaa gta tca ggc ggg 499
Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly Glu Val Ser Gly Gly
                        120 125 130

cag cgc caa cgc gcc ctc ata gcg caa ggt tta gcg caa cag gcg ccc 547
Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu Ala Gln Gln Ala Pro
                        135 140 145

tta ttg ctt ctc gac gaa ccc ctc gcc gcc gtg gac tcc cac gcg gca 595
Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val Asp Ser His Ala Ala
                        150 155 160 165

agt ctt atc gaa gat gtc att aac caa caa cgc aac caa gga acc aca 643
Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg Asn Gln Gly Thr Thr
                        170 175 180

att att ctt gcg act cac gat ctt gat caa gca cat caa gca gat cag 691
Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala His Gln Ala Asp Gln
                        185 190 195

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gaa tca ata aag aag cgt taataaaagtt tgacttgtgc ctc 780  
Glu Ser Ile Lys Lys Arg  
215

[illegible]

$\langle 210 \rangle$	251
$\langle 211 \rangle$	972
$\langle 212 \rangle$	DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXN02442

<400> 251

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gccgtgatgt tgttgagcgc gatgtgattg ccgtatgtgc atgtgagatt ccggacgctg 60
agttctgcca ttccttaatg ataacggtta tcattttcaa atg aag ttt ttt act 115
                                         Met Lys Phe Phe Thr
                                         1           5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg 163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
              10              15              20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg 211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
              25              30              35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc 259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
              40              45              50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg 307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
              55              60              65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg 355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
              70              75              80              85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa 403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
              90              95              100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat 451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
              105              110              115

tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc 499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly
              120              125              130

gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt 547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
              135              140              145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc 595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
              150              155              160              165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac 643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
              170              175              180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag 691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
              185              190              195

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gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc 739  
 Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala  
           200                                  205                                  210

acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg 787  
 Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met  
           215                                  220                                  225

atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta 835  
 Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu  
           230                                  235                                  240                                  245

atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta 883  
 Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu  
                                   250                                  255                                  260

agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt 931  
 Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser  
                                   265                                  270                                  275

agg tta aac ttc acc gcg tgatactgaa agacattttc aat 972  
 Arg Leu Asn Phe Thr Ala  
                                   280

<210> 252  
 <211> 283  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 252  
 Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe  
   1                                  5                                  10                                  15

Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser  
                                   20                                  25                                  30

Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp  
                                   35                                  40                                  45

Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu  
                                   50                                  55                                  60

Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser  
                                   65                                  70                                  75                                  80

Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val  
                                   85                                  90                                  95

Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile  
                                   100                                  105                                  110

Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe  
                                   115                                  120                                  125

Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile  
                                   130                                  135                                  140

Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe  
                                   145                                  150                                  155                                  160

Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn  
 165 170 175

Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr  
 180 185 190

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu  
 195 200 205

Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser  
 210 215 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile  
 225 230 235 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala  
 245 250 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr  
 260 265 270

Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala  
 275 280

<210> 253  
 <211> 972  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(949)  
 <223> FRXA02442

<400> 253  
 gccgtgatgt tgttgagcgc gatgtgattg ccgtatgtgc atgtgagatt ccggacgctg 60

agttctgcca ttccttaatg ataacgggta tcattttcaa atg aag ttt ttt act 115  
 Met Lys Phe Phe Thr  
 1 5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg 163  
 Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu  
 10 15 20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg 211  
 Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp  
 25 30 35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc 259  
 Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly  
 40 45 50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg 307  
 Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met  
 55 60 65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg 355  
 Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp



70	75	80	85	
acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa				403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln	90	95	100	
ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat				451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp	105	110	115	
tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc				499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly	120	125	130	
gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt				547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly	135	140	145	
gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc				595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe	150	155	160	165
gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac				643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His	170	175	180	
cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag				691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln	185	190	195	
gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc				739
Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala	200	205	210	
acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg				787
Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met	215	220	225	
atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta				835
Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu	230	235	240	245
atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta				883
Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu	250	255	260	
agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt				931
Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser	265	270	275	
agg tta aac ttc acc gcg tgatactgaa agacattttc aat				972
Arg Leu Asn Phe Thr Ala	280			

&lt;210&gt; 254

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 254

Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe  
 1 5 10 15  
 Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser  
 20 25 30  
 Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp  
 35 40 45  
 Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu  
 50 55 60  
 Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser  
 65 70 75 80  
 Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val  
 85 90 95  
 Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile  
 100 105 110  
 Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe  
 115 120 125  
 Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile  
 130 135 140  
 Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe  
 145 150 155 160  
 Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn  
 165 170 175  
 Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr  
 180 185 190  
 Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu  
 195 200 205  
 Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser  
 210 215 220  
 Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile  
 225 230 235 240  
 Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala  
 245 250 255  
 Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr  
 260 265 270  
 Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala  
 275 280

&lt;210&gt; 255

&lt;211&gt; 1431

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1408)

&lt;223&gt; RXA01756

&lt;400&gt; 255

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gcgcctgaaa tcgggcttgt tgagggggaga ggtgtgtgac atg aaa gag ttg gaa 115
                                   Met Lys Glu Leu Glu
                                   1 5

ctg ggc gag gcg agg gac gtc gct gca acg ttg gaa gcg atg ccg atc 163
Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu Glu Ala Met Pro Ile
                                   10 15 20

cag gag gtt att gat cag gtt gag cga act tct ata act aaa ggt gcg 211
Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser Ile Thr Lys Gly Ala
                                   25 30 35

gta ctg ctg cgt ctg ctc agt aaa gat cga tcg ttg ttg gtc ttc gat 259
Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser Leu Leu Val Phe Asp
                                   40 45 50

gct ctt ggt ccg cga ctc cag gct gat ctc att ggt gct ttt cag gat 307
Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile Gly Ala Phe Gln Asp
                                   55 60 65

gcg gaa gtg ctg gat tat ttc gct gac ctt gac cct gat gac cgc gtt 355
Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp Pro Asp Asp Arg Val
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tca ctg ctt gat gag ctg ccg gcg tcg atc gct gac gag ttg ctt cgc 403
Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala Asp Glu Leu Leu Arg
                                   90 95 100

agt ctc gat ccg cag gaa aag cag gtc acg gag ctg gtc ttg ggt tac 451
Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu Leu Val Leu Gly Tyr
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gca aag ggg tcg gtt gga cgt tgg atg tcg ccc cag gtt tta ttg ctt 499
Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro Gln Val Leu Leu Leu
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Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp Phe Val Arg Asn His
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gct gct gag gct gag acg att tat gcc tta cct att gtg aac cgt gct 595
Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro Ile Val Asn Arg Ala
                                   150 155 160 165

cgc caa gtg atg ggc gtg gtg tcg ttg cga aag ctg ttc atc gca gat 643
Arg Gln Val Met Gly Val Val Ser Leu Arg Lys Leu Phe Ile Ala Asp
                                   170 175 180

ccc act cta aaa gtc tcg gaa atc atg gtg cgt cct gtt tcg gtg ttg 691
Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg Pro Val Ser Val Leu
                                   185 190 195

gcg tcc gcg gat att gaa gaa acc gcc cgc tgg ttc cta cag ttg gac 739
Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp Phe Leu Gln Leu Asp

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200	205	210	
ctc gtt gcg atg ccc gtt gtg gat gaa tcg aac atg ctc tta gga gtg Leu Val Ala Met Pro Val Val Asp Glu Ser Asn Met Leu Leu Gly Val 215 220 225			787
ctg acc ttc gat gat gcg caa gac atc gtg gag caa gcc gac tct gag Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu Gln Ala Asp Ser Glu 230 235 240 245			835
gac tcc gct cgc agt ggt ggt tcg gaa cct ctc cag cag ccg tat cta Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu Gln Gln Pro Tyr Leu 250 255 260			883
tcc acg ccg att cgg aaa ctg gtg aag tcc cgc atc gta tgg ctt ctg Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg Ile Val Trp Leu Leu 265 270 275			931
gtt ttg gca gtg tca gca att ttg acg gtt caa gtt ctt gat att ttc Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln Val Leu Asp Ile Phe 280 285 290			979
gaa gcc acc ttg gtt gaa gcc gtg gta ctg gca ttg ttc att cct ttg Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala Leu Phe Ile Pro Leu 295 300 305			1027
ctc act ggt act ggc gga aac acc gga aac caa gct gca aca acc gtg Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln Ala Ala Thr Thr Val 310 315 320 325			1075
acc cgt gcg ctc gca ttg ggt gac gtc cga aaa tca gat gtc ttc cgc Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys Ser Asp Val Phe Arg 330 335 340			1123
gtc ttg ggc aga gaa atc cga gtc ggc ctc atg ctc ggg gca ttg ttg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met Leu Gly Ala Leu Leu 345 350 355			1171
ggt gcc gtt gga ttt gtg atc gca tcg ctt gtt tac ggc atg ccc gta Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val Tyr Gly Met Pro Val 360 365 370			1219
ggc act gtc atc ggt ctg aca ttg ttg gcg gtg tgc acg atg gcc gca Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val Cys Thr Met Ala Ala 375 380 385			1267
tca gtt ggc gga gta atg cca att att gcc aag gcg atc gga gcg gac Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys Ala Ile Gly Ala Asp 390 395 400 405			1315
cca gcg gtg ttc tct aat cct ttt att tca acc ttc tgt gat gca aca Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr Phe Cys Asp Ala Thr 410 415 420			1363
ggt ttg atc atc tac ttt gca att gcc aag ttg gtg ctc gga atc Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu Val Leu Gly Ile 425 430 435			1408
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Ile	Thr	Lys	Gly	Ala	Val	Leu	Leu	Arg	Leu	Leu	Ser	Lys	Asp	Arg	Ser
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Leu	Leu	Val	Phe	Asp	Ala	Leu	Gly	Pro	Arg	Leu	Gln	Ala	Asp	Leu	Ile
	50					55					60				
Gly	Ala	Phe	Gln	Asp	Ala	Glu	Val	Leu	Asp	Tyr	Phe	Ala	Asp	Leu	Asp
	65				70				75					80	
Pro	Asp	Asp	Arg	Val	Ser	Leu	Leu	Asp	Glu	Leu	Pro	Ala	Ser	Ile	Ala
				85					90					95	
Asp	Glu	Leu	Leu	Arg	Ser	Leu	Asp	Pro	Gln	Glu	Lys	Gln	Val	Thr	Glu
		100						105					110		
Leu	Val	Leu	Gly	Tyr	Ala	Lys	Gly	Ser	Val	Gly	Arg	Trp	Met	Ser	Pro
	115						120					125			
Gln	Val	Leu	Leu	Leu	Phe	Asp	Asp	Met	Ser	Val	Ala	Glu	Val	Leu	Asp
	130					135					140				
Phe	Val	Arg	Asn	His	Ala	Ala	Glu	Ala	Glu	Thr	Ile	Tyr	Ala	Leu	Pro
145					150					155				160	
Ile	Val	Asn	Arg	Ala	Arg	Gln	Val	Met	Gly	Val	Val	Ser	Leu	Arg	Lys
			165						170					175	
Leu	Phe	Ile	Ala	Asp	Pro	Thr	Leu	Lys	Val	Ser	Glu	Ile	Met	Val	Arg
			180					185					190		
Pro	Val	Ser	Val	Leu	Ala	Ser	Ala	Asp	Ile	Glu	Glu	Thr	Ala	Arg	Trp
		195					200						205		
Phe	Leu	Gln	Leu	Asp	Leu	Val	Ala	Met	Pro	Val	Val	Asp	Glu	Ser	Asn
	210					215						220			
Met	Leu	Leu	Gly	Val	Leu	Thr	Phe	Asp	Asp	Ala	Gln	Asp	Ile	Val	Glu
225					230					235				240	
Gln	Ala	Asp	Ser	Glu	Asp	Ser	Ala	Arg	Ser	Gly	Gly	Ser	Glu	Pro	Leu
			245						250					255	
Gln	Gln	Pro	Tyr	Leu	Ser	Thr	Pro	Ile	Arg	Lys	Leu	Val	Lys	Ser	Arg
		260						265					270		
Ile	Val	Trp	Leu	Leu	Val	Leu	Ala	Val	Ser	Ala	Ile	Leu	Thr	Val	Gln
		275					280					285			
Val	Leu	Asp	Ile	Phe	Glu	Ala	Thr	Leu	Val	Glu	Ala	Val	Val	Leu	Ala

290	295	300
Leu Phe Ile Pro Leu Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln 305 310 315 320		
Ala Ala Thr Thr Val Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys 325 330 335		
Ser Asp Val Phe Arg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met 340 345 350		
Leu Gly Ala Leu Leu Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val 355 360 365		
Tyr Gly Met Pro Val Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val 370 375 380		
Cys Thr Met Ala Ala Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys 385 390 395 400		
Ala Ile Gly Ala Asp Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr 405 410 415		
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Val Leu Gly Ile 435		

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 <211> 1142  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1119)  
 <223> RXA02068

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ggt gaa ttg cag gtc atg ggc gat att gtg ggt gca aaa gta cat acc Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr 35 40 45	144
gat gat cca gag ctg caa caa ttc cac ggt cgc gcg gta gaa atc gcc Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala 50 55 60	192
gat gtg gag ctg gag tta tcg cgc act cgc gat tgg atc atc acg cgc Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg 65 70 75 80	240

gtg gcg gtg ctg ggt gag cgc cct aaa ttt ggc cgg cgc cca gtg ctg	288
Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu	
85 90 95	
cac aca gtg ccg tgg agt cat atc cac ggc atc acc gca ggt ggt gtc	336
His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val	
100 105 110	
ggc gag tcc aat cac acc gcc gaa ctc atc gca ggg ttt gag gat atg	384
Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met	
115 120 125	
agg cct gcg gac gtc gca aag cag ctt tat cag ctg cct acg gct cag	432
Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln	
130 135 140	
cgt acc gaa gtg acg gaa gag ctt gac gac gaa aag ctg gcg gat atc	480
Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile	
145 150 155 160	
ctg cag gaa ttg tcc gag gac cgc caa gcc gag ttg att gaa gaa tta	528
Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu	
165 170 175	
gac atc gaa cgt gcc gcg gac att ctg gag gaa atg gat cca gat gat	576
Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp	
180 185 190	
gct gca gac ttg ttg ggt gag ctg cct gat gac aaa gct gat gtg ttg	624
Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu	
195 200 205	
ttg gat ctg atg gac cct gag gaa tct gcg ccg gtg cgt cgt ttg atg	672
Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met	
210 215 220	
gat ttc tcc ccg gac acc gtt ggt gcg ctg atg act cct gag cca tta	720
Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu	
225 230 235 240	
att atg gat cct tcc acc aca gtc gct gaa gcg ttg gcg atg gcc aga	768
Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg	
245 250 255	
aac ccc gac ctt cct act tct ttg gca tcg ttg atc ttt gtg gtg cgc	816
Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg	
260 265 270	
cca ccc acg gcc acg cct act gga aaa tac ctc ggc tgc gtg cat ctg	864
Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu	
275 280 285	
cag aaa ctg ctt ccg gag cct cca tca agt ttg att ggt ggc atc ctc	912
Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu	
290 295 300	
gac ccc gat ctg cca ccg ctc tac gct gat gat tct caa gaa acc gca	960
Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala	
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gct cga ttc ttt gcc acc tac aac ttg gtg tgc ggc ccc gtc ttg gat	1008

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<212> PRT
<213> Corynebacterium glutamicum
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Gly	Glu	Leu	Gln	Val	Met	Gly	Asp	Ile	Val	Gly	Ala	Lys	Val	His	Thr
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	50					55					60				
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Val	Ala	Val	Leu	Gly	Glu	Arg	Pro	Lys	Phe	Gly	Arg	Arg	Pro	Val	Leu
				85					90					95	
His	Thr	Val	Pro	Trp	Ser	His	Ile	His	Gly	Ile	Thr	Ala	Gly	Gly	Val
			100					105					110		
Gly	Glu	Ser	Asn	His	Thr	Ala	Glu	Leu	Ile	Ala	Gly	Phe	Glu	Asp	Met
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Arg	Pro	Ala	Asp	Val	Ala	Lys	Gln	Leu	Tyr	Gln	Leu	Pro	Thr	Ala	Gln
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Arg	Thr	Glu	Val	Thr	Glu	Glu	Leu	Asp	Asp	Glu	Lys	Leu	Ala	Asp	Ile
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Leu	Gln	Glu	Leu	Ser	Glu	Asp	Arg	Gln	Ala	Glu	Leu	Ile	Glu	Glu	Leu
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Asp	Ile	Glu	Arg	Ala	Ala	Asp	Ile	Leu	Glu	Glu	Met	Asp	Pro	Asp	Asp
			180					185					190		
Ala	Ala	Asp	Leu	Leu	Gly	Glu	Leu	Pro	Asp	Asp	Lys	Ala	Asp	Val	Leu
		195					200					205			



Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met  
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 Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu  
 225 230 235 240  
 Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg  
 245 250 255  
 Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg  
 260 265 270  
 Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu  
 275 280 285  
 Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu  
 290 295 300  
 Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala  
 305 310 315 320  
 Ala Arg Phe Phe Ala Thr Tyr Asn Leu Val Cys Gly Pro Val Leu Asp  
 325 330 335  
 Glu Asn Arg His Leu Leu Gly Ala Val Ala Val Asp Asp Leu Leu Asp  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 Met Ser Ser Ser Thr  
 1 5  
 ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg 163  
 Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr  
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 Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala  
 25 30 35  
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 Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro

40										45										50										
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Met	Val	Ala	Met	Leu	Leu	Val	Pro	Thr	Ile	Phe	Gly	Leu	Ile	Ala	Gly															
55					60					65																				
gca	gga	ctc	ggc	ctt	ggg	gac	atg	gcg	ctt	gac	gcc	atc	aag	gac	atg	355														
Ala	Gly	Leu	Gly	Leu	Gly	Asp	Met	Ala	Leu	Asp	Ala	Ile	Lys	Asp	Met															
70					75					80					85															
gcg	cct	acc	gcg	gca	ctc	ctg	atg	ttc	gcg	att	atg	ttc	ttc	gga	atc	403														
Ala	Pro	Thr	Ala	Ala	Leu	Leu	Met	Phe	Ala	Ile	Met	Phe	Phe	Gly	Ile															
90					95					100																				
atg	atc	gac	gtc	gga	ctc	ttc	gac	ccc	ctg	atc	cgc	gtg	atc	acc	cgc	451														
Met	Ile	Asp	Val	Gly	Leu	Phe	Asp	Pro	Leu	Ile	Arg	Val	Ile	Thr	Arg															
105					110					115																				
gtt	ctt	cac	gat	gac	ccc	gca	aag	gtc	gtc	atc	ggc	acc	gca	gta	ctt	499														
Val	Leu	His	Asp	Asp	Pro	Ala	Lys	Val	Val	Ile	Gly	Thr	Ala	Val	Leu															
120					125					130																				
gca	ggg	gtt	gtc	tcc	ctc	gac	ggc	gac	ggc	tcc	acc	acc				538														
Ala	Gly	Val	Val	Ser	Leu	Asp	Gly	Asp	Gly	Ser	Thr	Thr																		
135					140					145																				

&lt;210&gt; 260

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 260

Met	Ser	Ser	Ser	Thr	Leu	Leu	Leu	Ala	Ser	Gly	Gln	Val	Thr	Ala	Leu
1				5					10					15	

Ala	Ala	Asp	Tyr	Thr	Leu	Ser	His	Thr	Pro	Ser	Asp	Gly	Ile	Leu	Val
		20						25					30		

Val	Leu	Gly	Phe	Ala	Met	Ile	Leu	Thr	Phe	Met	Thr	Leu	Ile	Met	Leu
		35					40					45			

Gly	Arg	Leu	Thr	Pro	Met	Val	Ala	Met	Leu	Leu	Val	Pro	Thr	Ile	Phe
	50					55					60				

Gly	Leu	Ile	Ala	Gly	Ala	Gly	Leu	Gly	Leu	Gly	Asp	Met	Ala	Leu	Asp
	65				70				75					80	

Ala	Ile	Lys	Asp	Met	Ala	Pro	Thr	Ala	Ala	Leu	Leu	Met	Phe	Ala	Ile
			85						90					95	

Met	Phe	Phe	Gly	Ile	Met	Ile	Asp	Val	Gly	Leu	Phe	Asp	Pro	Leu	Ile
			100					105					110		

Arg	Val	Ile	Thr	Arg	Val	Leu	His	Asp	Asp	Pro	Ala	Lys	Val	Val	Ile
		115					120					125			

Gly	Thr	Ala	Val	Leu	Ala	Gly	Val	Val	Ser	Leu	Asp	Gly	Asp	Gly	Ser
	130					135					140				

Thr Thr

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<210> 261
<211> 281
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(258)  
<223> RXA02808
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<400> 261																			
ttt	tac	ttc	ggc	atc	ctc	cca	gtc	ctt	gca	gaa	agt	gct	tcc	cac	ttc	48			
Phe	Tyr	Phe	Gly	Ile	Leu	Pro	Val	Leu	Ala	Glu	Ser	Ala	Ser	His	Phe				
1				5				10						15					
ggc	atc	gag	cct	gtg	gaa	atg	gcc	cgc	gca	tcc	atc	act	ggc	cag	ccc	96			
Gly	Ile	Glu	Pro	Val	Glu	Met	Ala	Arg	Ala	Ser	Ile	Thr	Gly	Gln	Pro				
			20				25						30						
gtt	cac	atg	caa	agc	ccg	ctg	gtc	cca	gcg	atc	ctc	ctg	ctg	gtt	tcc	144			
Val	His	Met	Gln	Ser	Pro	Leu	Val	Pro	Ala	Ile	Leu	Leu	Leu	Val	Ser				
			35				40						45						
ctc	gcc	aac	gtc	aac	ctt	ggc	gac	cac	cac	aag	aag	gtt	ctg	tgg	cgc	192			
Leu	Ala	Asn	Val	Asn	Leu	Gly	Asp	His	His	Lys	Lys	Val	Leu	Trp	Arg				
50						55						60							
gcc	tgc	atc	gtg	tcc	atc	gcg	atg	ctc	gcc	gta	gcc	ctc	ttc	atc	ggc	240			
Ala	Cys	Ile	Val	Ser	Ile	Ala	Met	Leu	Ala	Val	Ala	Leu	Phe	Ile	Gly				
65						70				75				80					
gtc	gtg	cca	ctc	agc	gca	taaaaatagct					tttcgacgcc					aaa	281		
Val	Val	Pro	Leu	Ser	Ala														
			85																

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<210> 262
<211> 86
<212> PRT
<213> Corynebacterium glutamicum
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<400> 262
Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
  1             5             10             15

Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
          20             25             30

Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
          35             40             45

Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
          50             55             60

Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
  65             70             75             80

Val Val Pro Leu Ser Ala

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<210> 263
<211> 960
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(937)
<223> RXN00444
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ttcctcagca gcgatcgtgc caaggagatc cttgccagct atg gtt ttg gca caa 115  
Met Val Leu Ala Gln  
1 5

act aaa aag gct cgt cga agc gag aat cat atc ctc cca ggg tgg ttg 163  
Thr Lys Lys Ala Arg Ser Glu Asn His Ile Leu Pro Gly Trp Leu  
10 15 20

ctc atc cca gcc acc ctg gcc atg ctg ctg atc att gga cct att ttt 211  
Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile Phe  
25 30 35

gct ttg ctg ttg cag atc ccc tgg gat cgg tct tgg gag ttg ctt acc 259  
Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu Thr  
40 45 50

gcg ccg gaa tct tta gga acc gca cgg tta tct atc gga act gct ctg 307  
Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala Leu  
55 60 65

ttt tct acc gcg cta tgc gca att gtg ggt ttc ccg cta gcg ttg gcg 355  
Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu Ala  
70 75 80 85

ctg cat tta tat gag cgt tcg cac ccc agg gtg aca tca gtt ttg acg 403  
Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu Thr  
90 95 100

gtg ctg gtt tat gcg cct ttg gtg ttg tgc ccg gtg gtg tct ggt ttg 451  
Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu  
105 110 115

gcg ctg act ttt ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt 499  
Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp Leu  
120 125 130

gat cag gtt gga ttg ccg att gca ttt acc acc acg gct gtg gtg ttt 547  
Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe  
135 140 145

gcc cag gtg ttt gta gcg ttg cca ttt ttc att tcc act gtg act act 595  
Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr  
150 155 160 165

gca ctg cgt ggc att cca aaa cag ttt gag gaa atc gca gct act gaa 643

Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu  
 170 175 180

ggc gca acc cgc tgg gag atc atg cac aag atg atc att ccg ctg gcg 691  
 Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala  
 185 190 195

atg cct gga att ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg 739  
 Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu  
 200 205 210

ggc gag tat ggt gcg aca ctg act ttt gct gga aat att gca ggt gtt 787  
 Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val  
 215 220 225

acc cgc acc att ccg ttg cat att gag ctt ggt ttg agt tcc aat gac 835  
 Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp  
 230 235 240 245

atg gat aaa gcc ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc 883  
 Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val  
 250 255 260

ctc atc att gga gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga 931  
 Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg  
 265 270 275

aag gtt taattgatgt ctggttcgcc gga 960  
 Lys Val

&lt;210&gt; 264

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 264

Met Val Leu Ala Gln Thr Lys Lys Ala Arg Arg Ser Glu Asn His Ile  
 1 5 10 15

Leu Pro Gly Trp Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile  
 20 25 30

Ile Gly Pro Ile Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser  
 35 40 45

Trp Glu Leu Leu Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser  
 50 55 60

Ile Gly Thr Ala Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe  
 65 70 75 80

Pro Leu Ala Leu Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val  
 85 90 95

Thr Ser Val Leu Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro  
 100 105 110

Val Val Ser Gly Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe  
 115 120 125

Leu Gly Ser Trp Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr  
 130 135 140  
 Thr Ala Val Val Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile  
 145 150 155 160  
 Ser Thr Val Thr Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu  
 165 170 175  
 Ile Ala Ala Thr Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met  
 180 185 190  
 Ile Ile Pro Leu Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly  
 195 200 205  
 Phe Ala Arg Ala Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly  
 210 215 220  
 Asn Ile Ala Gly Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly  
 225 230 235 240  
 Leu Ser Ser Asn Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu  
 245 250 255  
 Leu Ala Val Tyr Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu  
 260 265 270  
 Phe Ser Lys Val Arg Lys Val  
 275

<210> 265  
 <211> 900  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(877)  
 <223> FRXA00444

<220>  
 <223> All occurrences of n = any nucleotide

<400> 265  
 gatcgtgccca aggagatcct tgccagcnnn nnnntnnna ntgggttttg cacaactaa 60

aaaggctcgt cgaagcgaga atcatatcct ccaggggtgg ttg ctc atc cca gcc 115  
 Leu Leu Ile Pro Ala  
 1 5

acc ctg gcc atg ctg ctg atc att gga cct att ttt gct ttg ctg ttg 163  
 Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile Phe Ala Leu Leu Leu  
 10 15 20

cag atc ccc tgg gat cgg tct tgg gag ttg ctt acc gcg ccg gaa tct 211  
 Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu Thr Ala Pro Glu Ser  
 25 30 35

tta gga acc gca cgg tta tct atc gga act gct ctg ttt tct acc gcg 259

Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala Leu Phe Ser Thr Ala	
40 45 50	
cta tgc gca att gtg ggt ttc ccg cta gcg ttg gcg ctg cat tta tat	307
Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu Ala Leu His Leu Tyr	
55 60 65	
gag cgt tgc cac ccc agg gtg aca tca gtt ttg acg gtg ctg gtt tat	355
Glu Arg Ser His Pro Arg Val Thr Ser Val Leu Thr Val Leu Val Tyr	
70 75 80 85	
gcg cct ttg gtg ttg tgc ccg gtg gtg tct ggt ttg gcg ctg act ttt	403
Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu Ala Leu Thr Phe	
90 95 100	
ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt gat cag gtt gga	451
Leu Trp Gly Arg Gly Phe Leu Gly Ser Trp Leu Asp Gln Val Gly	
105 110 115	
ttg ccg att gca ttt acc acc acg gct gtg gtg ttt gcc cag gtg ttt	499
Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe Ala Gln Val Phe	
120 125 130	
gta gcg ttg cca ttt ttc att tcc act gtg act act gca ctg cgt ggc	547
Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr Ala Leu Arg Gly	
135 140 145	
att cca aaa cag ttt gag gaa atc gca gct act gaa ggc gca acc cgc	595
Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu Gly Ala Thr Arg	
150 155 160 165	
tgg gag atc atg cac aag atg atc att ccg ctg gcg atg cct gga att	643
Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala Met Pro Gly Ile	
170 175 180	
ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg ggc gag tat ggt	691
Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu Gly Glu Tyr Gly	
185 190 195	
gcg aca ctg act ttt gct gga aat att gca ggt gtt acc cgc acc att	739
Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val Thr Arg Thr Ile	
200 205 210	
ccg ttg cat att gag ctt ggt ttg agt tcc aat gac atg gat aaa gcc	787
Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp Met Asp Lys Ala	
215 220 225	
ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc ctc atc att gga	835
Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val Leu Ile Ile Gly	
230 235 240 245	
gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga aag gtt	877
Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg Lys Val	
250 255	
taattgatgt ctggttcgcc gga	900

&lt;210&gt; 266

&lt;211&gt; 259

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 266

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Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile
 1              5              10              15

Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu
      20              25              30

Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala
      35              40              45

Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu
 50              55              60

Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu
 65              70              75              80

Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly
      85              90              95

Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp
 100              105              110

Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val
 115              120              125

Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr
 130              135              140

Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr
 145              150              155              160

Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu
      165              170              175

Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala
      180              185              190

Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly
 195              200              205

Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn
 210              215              220

Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr
 225              230              235              240

Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val
      245              250              255

Arg Lys Val

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<210> 267

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>



<221> CDS  
 <222> (101)..(829)  
 <223> RXN02614

<400> 267

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acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
                               Met Thr Ala Thr Leu
                               1                               5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
                               10                               15                               20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
                               25                               30                               35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
                               40                               45                               50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
                               55                               60                               65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
                               70                               75                               80                               85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
                               90                               95                               100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
                               105                               110                               115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
                               120                               125                               130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
                               135                               140                               145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
                               150                               155                               160                               165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
                               170                               175                               180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
                               185                               190                               195

gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr

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200	205	210	
gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac			787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr			
215	220	225	
acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc			829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala			
230	235	240	
tagaaagaaa tcatgaaatt taa			852

<210> 268  
 <211> 243  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 268  
 Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu  
 1 5 10 15  
 Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr  
 20 25 30  
 Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly  
 35 40 45  
 Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser  
 50 55 60  
 Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro  
 65 70 75 80  
 Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu  
 85 90 95  
 Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala  
 100 105 110  
 Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu  
 115 120 125  
 Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu  
 130 135 140  
 Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu  
 145 150 155 160  
 Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val  
 165 170 175  
 Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu  
 180 185 190  
 Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile  
 195 200 205  
 Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro  
 210 215 220

Thr Pro Ala

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<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02614
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<400> 269																																
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acaccttccg		ctaccgaaac		gcataagaaa		gttgctcgcc		atg		act		gcc		aca		ttg		115														
										Met		Thr		Ala		Thr		Leu	5													
										1																						
tca		ctc		aaa		ccc		gca		gcc		act		gtc		cgt		gga		ttg		cgc		aaa		tca		tac		gga		163
Ser		Leu		Lys		Pro		Ala		Ala		Thr		Val		Arg		Gly		Leu		Arg		Lys		Ser		Tyr		Gly		
						10										15												20				
act		aaa		gaa		gtc		ctc		caa		gga		atc		gac		ctc		acc		atc		aac		tgc		ggc		gaa		211
Thr		Lys		Glu		Val		Leu		Gln		Gly		Ile		Asp		Leu		Thr		Ile		Asn		Cys		Gly		Glu		
						25										30										35						
gta		acc		gcg		ctg		atc		gga		cgc		tca		ggc		tca		gga		aaa		tcc		acc		atc		ctg		259
Val		Thr		Ala		Leu		Ile		Gly		Arg		Ser		Gly		Ser		Gly		Lys		Ser		Thr		Ile		Leu		
						40								45										50								
cgc		gtg		ttg		gcg		ggc		cta		tct		aaa		gag		cat		tcc		ggc		tct		gta		gaa		att		307
Arg		Val		Leu		Ala		Gly		Leu		Ser		Lys		Glu		His		Ser		Gly		Ser		Val		Glu		Ile		
		55										60										65										
tcc		gga		aac		ccg		gcc		gtt		gcc		ttc		caa		gag		cct		cgc		ctg		ttg		ccg		tgg		355
Ser		Gly		Asn		Pro		Ala		Val		Ala		Phe		Gln		Glu		Pro		Arg		Leu		Leu		Pro		Trp		
		70						75								80												85				
aaa		acg		gtg		ctc		gat		aat		gtg		acc		ttt		ggc		ctc		aac		cgc		act		gat		att		403
Lys		Thr		Val		Leu		Asp		Asn		Val		Thr		Phe		Gly		Leu		Asn		Arg		Thr		Asp		Ile		
								90										95										100				
tcc		tgg		tca		gaa		gca		caa		gaa		cgc		gcc		tcg		gca		ctg		ctt		gca		gaa		gtc		451
Ser		Trp		Ser		Glu		Ala		Gln		Glu		Arg		Ala		Ser		Ala		Leu		Leu		Ala		Glu		Val		

Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg  
 150 155 160 165  
 ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643  
 Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu  
 170 175 180  
 gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691  
 Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala  
 185 190 195  
 gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739  
 Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr  
 200 205 210  
 gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac 787  
 Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr  
 215 220 225  
 acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc 829  
 Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala  
 230 235 240  
 tagaaagaaa tcatgaaatt taa 852

<210> 270  
 <211> 243  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 270  
 Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu  
 1 5 10 15  
 Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr  
 20 25 30  
 Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly  
 35 40 45  
 Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser  
 50 55 60  
 Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro  
 65 70 75 80  
 Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu  
 85 90 95  
 Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala  
 100 105 110  
 Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu  
 115 120 125  
 Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu  
 130 135 140  
 Ile Ser Glu Pro Glu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu  
 145 150 155 160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val  
165 170 175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu  
180 185 190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile  
195 200 205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro  
210 215 220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr  
225 230 235 240

Thr Pro Ala

<210> 271

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXN01142

<400> 271

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ccgaggcatg gttttccaag accacgcct cctgccctga ttg acc gca cgc ggc 115  
Leu Thr Ala Arg Gly  
1 5

aac atc gac ttc ggg ctc cgc tcc gcg cgc ccc tcc ttg agc aaa acc 163  
Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro Ser Leu Ser Lys Thr  
10 15 20

gaa cgc gcc gac atc acc cgc acc cac ctc gaa caa gta ggc ctc acc 211  
Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr  
25 30 35

gac gcc gcc gaa cgg cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag 259  
Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln  
40 45 50

cga gtc ggc atc gca cgc gcc ttc gcc atc gac cca cca atc atg ctt 307  
Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu  
55 60 65

ctc gac gaa ccc ttc ggc gcc ctc gac gcc ctc acc cgc cgc gaa ctc 355  
Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu  
70 75 80 85

cag ctc caa cta ctc aac att tgg gaa gcc tcc cgc cgc acc gtc gtc 403  
Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val  
90 95 100

atg gtc acc cac gac gtc gac gag gcc atc ctg ctc tcc gac cga gtt 451  
Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val  
105 110 115

ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca 499  
Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro  
120 125 130

gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt 547  
Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val  
135 140 145

gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag 595  
Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu  
150 155 160 165

cac tagtttctaa cacgtctttt aaa 621  
His

<210> 272

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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1 5 10 15

Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu  
20 25 30

Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser  
35 40 45

Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp  
50 55 60

Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu  
65 70 75 80

Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser  
85 90 95

Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu  
100 105 110

Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile  
115 120 125

Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser  
130 135 140

Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met  
145 150 155 160

Leu His Leu Leu Glu His  
165

<210> 273  
 <211> 443  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(420)  
 <223> FRXA01142

<400> 273  
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 Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg  
 1 5 10 15  
 cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag cga gtc ggc atc gca 96  
 Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala  
 20 25 30  
 cgc gcc ttc gcc atc gac cca cca atc atg ctt ctc gac gaa ccc ttc 144  
 Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe  
 35 40 45  
 gga gcc ctc gac gcc ctc acc cgc cgc gaa ctc cag ctc caa cta ctc 192  
 Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Leu  
 50 55 60  
 aac att tgg gaa gcc tcc cgc cgc acc gtc gtc atg gtc acc cac gac 240  
 Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp  
 65 70 75 80  
 gtc gac gag gcc atc ctg ctc tcc gac cga gtt ctc gtg atg tcc aag 288  
 Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys  
 85 90 95  
 agc ccc gaa gcc acc atc atc acc gat att cca gtg aat ctt ccc cgc 336  
 Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg  
 100 105 110  
 ccc aga cac gag ctg agt gaa gac gct tct gtt gaa gcc gag acc aca 384  
 Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr  
 115 120 125  
 gcc ctg cgt aag cgg atg ctg cat ctg ctg gag cac tagttttctaa 430  
 Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His  
 130 135 140  
 cacgtctttt aaa 443

<210> 274  
 <211> 140  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 274  
 Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg  
 1 5 10 15  
 Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala  
 20 25 30

Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe  
           35                                  40                                  45  
 Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu  
           50                                  55                                  60  
 Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp  
           65                                  70                                  75                                  80  
 Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys  
                                   85                                  90                                  95  
 Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg  
                                   100                                  105                                  110  
 Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr  
           115                                  120                                  125  
 Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His  
           130                                  135                                  140

&lt;210&gt; 275

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(925)

&lt;223&gt; RXN01141

&lt;400&gt; 275

aaagaacact cggtatggca cctgatttaa ggatgctgca atcgtgacac atatcctctt 60  
 cgacagcagg cgttttctgc aactgggcgc ttttgcgctcc ttg agc acc gca ttg 115  
   Leu Ser Thr Ala Leu  
   1                                  5  
 gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat gaa cct gcg 163  
 Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn Glu Pro Ala  
                                   10                                  15                                  20  
 gat aac act ccc ctg acc att ggc tac gtg cct att gcg ggc tcg gcg 211  
 Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala Gly Ser Ala  
                                   25                                  30                                  35  
 ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa cac ggc gtg 259  
 Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys His Gly Val  
           40                                  45                                  50  
 aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg tgg acc gcc 307  
 Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu Trp Thr Ala  
           55                                  60                                  65  
 tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg ccg atg act 355  
 Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser Pro Met Thr  
           70                                  75                                  80                                  85  
 gtg gcg att aat gct gga gtg acc aac gcg tcg cgc ccg acg gag ctg 403



Val	Ala	Ile	Asn	Ala	Gly	Val	Thr	Asn	Ala	Ser	Arg	Pro	Thr	Glu	Leu		
				90					95					100			
tcg	ttt	acc	cag	aac	acc	aat	ggg	caa	gca	att	acc	ttg	gcg	tca	aag	451	
Ser	Phe	Thr	Gln	Asn	Thr	Asn	Gly	Gln	Ala	Ile	Thr	Leu	Ala	Ser	Lys		
			105					110					115				
cac	tat	ggg	tcc	gtc	aat	tca	gcg	gcg	gat	ctt	aaa	ggc	atg	gtg	ctg	499	
His	Tyr	Gly	Ser	Val	Asn	Ser	Ala	Ala	Asp	Leu	Lys	Gly	Met	Val	Leu		
		120					125					130					
gga	att	cct	ttt	gaa	tat	tca	gtc	cat	gcg	ctg	ctc	ctg	cgc	gat	tat	547	
Gly	Ile	Pro	Phe	Glu	Tyr	Ser	Val	His	Ala	Leu	Leu	Leu	Arg	Asp	Tyr		
	135					140					145						
ctc	gtc	tca	aac	gca	gtt	gat	ccc	atc	gcc	gat	ctt	gag	ctt	cgc	ctg	595	
Leu	Val	Ser	Asn	Ala	Val	Asp	Pro	Ile	Ala	Asp	Leu	Glu	Leu	Arg	Leu		
150					155					160					165		
ctc	cga	cct	gcc	gat	atg	gtc	gca	caa	ttg	aca	gtt	gag	ggc	atc	gat	643	
Leu	Arg	Pro	Ala	Asp	Met	Val	Ala	Gln	Leu	Thr	Val	Glu	Gly	Ile	Asp		
			170					175						180			
gga	ttc	att	ggg	cct	ggg	ccg	ttt	aat	gaa	cgc	gcc	atc	agc	aat	ggc	691	
Gly	Phe	Ile	Gly	Pro	Gly	Pro	Phe	Asn	Glu	Arg	Ala	Ile	Ser	Asn	Gly		
		185						190					195				
tcc	ggc	cgg	att	tgg	ctg	ctg	acc	aaa	caa	ctg	tgg	gac	aaa	cat	cca	739	
Ser	Gly	Arg	Ile	Trp	Leu	Leu	Thr	Lys	Gln	Leu	Trp	Asp	Lys	His	Pro		
		200					205					210					
tgc	tgc	gcc	gtg	gcg	atg	gcc	aaa	gag	tgg	aaa	gct	gaa	cac	ccc	acg	787	
Cys	Cys	Ala	Val	Ala	Met	Ala	Lys	Glu	Trp	Lys	Ala	Glu	His	Pro	Thr		
	215					220					225						
gcg	gct	cag	ggg	gtg	ctt	aat	gcg	ctg	gag	gaa	gcc	tcc	gca	att	ttg	835	
Ala	Ala	Gln	Gly	Val	Leu	Asn	Ala	Leu	Glu	Glu	Ala	Ser	Ala	Ile	Leu		
230					235				240						245		
agc	aat	ccg	gca	caa	ttt	gat	tcc	tcg	gca	cgc	acg	ctg	tcg	cag	gaa	883	
Ser	Asn	Pro	Ala	Gln	Phe	Asp	Ser	Ser	Ala	Arg	Thr	Leu	Ser	Gln	Glu		
			250						255					260			
aaa	tac	ctc	aac	cag	cct	gcc	acg	ttg	ctg	gat	gga	ccg	tcg			925	
Lys	Tyr	Leu	Asn	Gln	Pro	Ala	Thr	Leu	Leu	Asp	Gly	Pro	Ser				
			265					270					275				
taatcatcgg	catcaccggc	tta														948	

<210> 276  
 <211> 275  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 276  
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 1 5 10 15  
 Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro  
 20 25 30

Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe  
                   35                                  40                                  45  
 Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser  
           50                                  55                                  60  
 Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met  
   65                                  70                                  75                                  80  
 Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser  
                   85                                  90                                  95  
 Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile  
                  100                                 105                                 110  
 Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu  
          115                                 120                                 125  
 Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu  
   130                                 135                                 140  
 Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp  
  145                                 150                                 155                                 160  
 Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr  
                  165                                 170                                 175  
 Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg  
                  180                                 185                                 190  
 Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu  
          195                                 200                                 205  
 Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys  
   210                                 215                                 220  
 Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu  
  225                                 230                                 235                                 240  
 Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg  
                  245                                 250                                 255  
 Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp  
                  260                                 265                                 270  
 Gly Pro Ser  
           275

<210> 277

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> FRXA01135

<400> 277

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gaacactcgg tatggcacct gatttaagga tgctgcaatc gtg aca cat atc ctc 115  
 Val Thr His Ile Leu  
 1 5

ttc gac agc agg cgt ttt ctg caa ctg ggc gct ttt gcg tcc ttg agc 163  
 Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala Phe Ala Ser Leu Ser  
 10 15 20

acc gca ttg gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat 211  
 Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn  
 25 30 35

gaa cct gcg gat aac act ccc ctg acc att ggc tac gtg cct att gcg 259  
 Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala  
 40 45 50

ggc tcg gcg cgg att gct atc gca gat gcg cta ggg ctg ttt aag aaa 307  
 Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys  
 55 60 65

cac ggc gtg aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg 355  
 His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu  
 70 75 80 85

tgg acc gcc tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg 403  
 Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser  
 90 95 100

ccg atg act gtg gcg att aat 424  
 Pro Met Thr Val Ala Ile Asn  
 105

&lt;210&gt; 278

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 278

Val Thr His Ile Leu Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala  
 1 5 10 15

Phe Ala Ser Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr  
 20 25 30

Ser Thr Ser Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly  
 35 40 45

Tyr Val Pro Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu  
 50 55 60

Gly Leu Phe Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser  
 65 70 75 80

Gly Trp Ser Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val  
 85 90 95

Ala His Met Leu Ser Pro Met Thr Val Ala Ile Asn  
 100 105

<210> 279  
 <211> 485  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(462)  
 <223> FRXA01141

<400> 279  
 gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg gga att cct ttt 48  
 Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe  
 1 5 10 15  
 gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat ctc gtc tca aac 96  
 Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn  
 20 25 30  
 gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg ctc cga cct gcc 144  
 Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala  
 35 40 45  
 gat atg gtc gca caa ttg aca gtt gag ggc atc gat gga ttc att ggg 192  
 Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly  
 50 55 60  
 cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc tcc ggc cgg att 240  
 Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile  
 65 70 75 80  
 tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca tgc tgc gcc gtg 288  
 Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val  
 85 90 95  
 gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg gcg gct cag ggt 336  
 Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly  
 100 105 110  
 gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg agc aat ccg gca 384  
 Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala  
 115 120 125  
 caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa aaa tac ctc aac 432  
 Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn  
 130 135 140  
 cag cct gcc acg ttg ctg gat gga ccg tcg taatcatcgg catcaccggc 482  
 Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser  
 145 150  
 tta 485

<210> 280  
 <211> 154  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 280

Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe  
 1 5 10 15

Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn  
 20 25 30

Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala  
 35 40 45

Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly  
 50 55 60

Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile  
 65 70 75 80

Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val  
 85 90 95

Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly  
 100 105 110

Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala  
 115 120 125

Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn  
 130 135 140

Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser  
 145 150

&lt;210&gt; 281

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(892)

&lt;223&gt; RXA00728

&lt;400&gt; 281

gattacttca cagatgtcag atcttaataca agggcctgga gcttcaacgg cccaaccgaa 60

accgattgaa gccaaagccac tacgccaccc tggccggtgg gtg gca gcc gct atc 115  
 Val Ala Ala Ala Ile  
 1 5

atc gtg gca ctg ctc gca tgg ttt atc atc agc gcg ctc aac aat gag 163  
 Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser Ala Leu Asn Asn Glu  
 10 15 20

gcc tac ggt tgg gat acc tac cgc tcg tat ctt ttt gac acc cgc att 211  
 Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu Phe Asp Thr Arg Ile  
 25 30 35

gcc acc gcg gca ctt cac acc att gcg ctg acc ttg ctg tcc atg atc 259  
 Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr Leu Leu Ser Met Ile  
 40 45 50

ttg ggt gtg gtt ctc ggc gca atc ttg gcc gtc atg cgt atg tcc ggc	307
Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val Met Arg Met Ser Gly	
55 60 65	
aac cct gtc atg cag ggc gta gcg tgg ctg tac ctg tgg att ttc cgc	355
Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr Leu Trp Ile Phe Arg	
70 75 80 85	
ggc acc cca att tat gtg cag ttg gtg ttc tgg ggc ctg ctg ggt tcc	403
Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp Gly Leu Leu Gly Ser	
90 95 100	
ttg tac cag tcg atc aac ctc ggt ttc gca gag atc gat ctg caa agc	451
Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu Ile Asp Leu Gln Ser	
105 110 115	
ttg ctg tct aat atg ttc ctg ctc gcg gtg atc ggt ctg ggt ctc aac	499
Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile Gly Leu Gly Leu Asn	
120 125 130	
gag gct gcg tac atg gcg gaa atc gtg cgc tcg ggc atc caa gcg gtg	547
Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser Gly Ile Gln Ala Val	
135 140 145	
cct gag ggc cag atg gag gcg tcg aaa gct ttg ggt atg aac tgg tca	595
Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu Gly Met Asn Trp Ser	
150 155 160 165	
atg acc atg cgt cgc acc atc ttg ccg cag gcc atg cgc atc atc att	643
Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala Met Arg Ile Ile Ile	
170 175 180	
ccg cca acc ggc aat gaa ctg atc tcc atg ctc aag acc acc tct ctg	691
Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu Lys Thr Thr Ser Leu	
185 190 195	
gtt gtt gcg att cct tat tct ctc gag ctg tac ggc cgc agc atg gat	739
Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr Gly Arg Ser Met Asp	
200 205 210	
att gcg tac tcc ctc ttc gag cca gtt cca atg ctt ctg gtt gct gcg	787
Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met Leu Leu Val Ala Ala	
215 220 225	
agc tgg tac ttg gtc atc acc tct att ctt atg gtt ggt cag tac tac	835
Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met Val Gly Gln Tyr Tyr	
230 235 240 245	
ctg gag aag cac ttc gaa aag ggc agc acc cgc acc ctg acc gca cgt	883
Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg Thr Leu Thr Ala Arg	
250 255 260	
cag ctc gct	892
Gln Leu Ala	

&lt;210&gt; 282

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Val Ala Ala Ala Ile Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser  
 1 5 10 15  
 Ala Leu Asn Asn Glu Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu  
 20 25 30  
 Phe Asp Thr Arg Ile Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr  
 35 40 45  
 Leu Leu Ser Met Ile Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val  
 50 55 60  
 Met Arg Met Ser Gly Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr  
 65 70 75 80  
 Leu Trp Ile Phe Arg Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp  
 85 90 95  
 Gly Leu Leu Gly Ser Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu  
 100 105 110  
 Ile Asp Leu Gln Ser Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile  
 115 120 125  
 Gly Leu Gly Leu Asn Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser  
 130 135 140  
 Gly Ile Gln Ala Val Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu  
 145 150 155 160  
 Gly Met Asn Trp Ser Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala  
 165 170 175  
 Met Arg Ile Ile Ile Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu  
 180 185 190  
 Lys Thr Thr Ser Leu Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr  
 195 200 205  
 Gly Arg Ser Met Asp Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met  
 210 215 220  
 Leu Leu Val Ala Ala Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met  
 225 230 235 240  
 Val Gly Gln Tyr Tyr Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg  
 245 250 255  
 Thr Leu Thr Ala Arg Gln Leu Ala  
 260

&lt;210&gt; 283

&lt;211&gt; 1518

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1495)

&lt;223&gt; RXA02663

&lt;400&gt; 283

gtgcaaatat ctgtccagtt cgtgagacta cgtcaatgct tccaaggtca ttggcgcac 60

aaccgctcac atcttgatca agcaagttgc ccgaaactgc atg gct ccg att ctg 115  
Met Ala Pro Ile Leu  
1 5

gtg ttc gcc acc gtc ctg gtc gcc gat gcg att gtc ttc gaa gca tcc 163  
Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile Val Phe Glu Ala Ser  
10 15 20

ctg tcc ttc atc aac gct ggt gtg aaa cca cca tca cct tca tgg ggc 211  
Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro Ser Pro Ser Trp Gly  
25 30 35

aac atc ctt gcc gat ggt aaa gcc ctg ctg ctt agc ggc gca tgg tgg 259  
Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu Ser Gly Ala Trp Trp  
40 45 50

cca acc ttc ttc cca ggt ttg atg atc ctg ctg acc gtt ctc tgc ttg 307  
Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu Thr Val Leu Cys Leu  
55 60 65

aac atc ctt tct gaa ggc ctc acc gac acc ctg gcc agc cct aag cca 355  
Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu Ala Ser Pro Lys Pro  
70 75 80 85

aag cct gtt tca gct tct gca aag aag gca ctg aag aag gaa gaa tcc 403  
Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu Lys Lys Glu Glu Ser  
90 95 100

ggt gaa aag gaa ggc tcc gga atc gtg ctt ggg cac acc aca cgt gaa 451  
Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly His Thr Thr Arg Glu  
105 110 115

gaa gcc aac gcc tca ctg ctc gca tca ctt gct gcg cta tcc acc agc 499  
Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala Ala Leu Ser Thr Ser  
120 125 130

gaa aac aat tcc aat aac cgg ctt ata ttt gat ggc aac ccc act cct 547  
Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp Gly Asn Pro Thr Pro  
135 140 145

ctg ttg gaa gtt cgc gat cta aag atc tcc ttc ccc aat gct cac gga 595  
Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe Pro Asn Ala His Gly  
150 155 160 165

gat atc aat att gtc gac ggc gtg aac ttc acc gtc gcc cca ggc caa 643  
Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr Val Ala Pro Gly Gln  
170 175 180

acc atg ggt ctt gtc ggt gaa tcc ggc tgt ggt aaa tcg att acc gca 691  
Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly Lys Ser Ile Thr Ala  
185 190 195

atg tcg atc atg ggt ctg ctg cct cca aca gca aag atc gaa ggc gag 739  
Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala Lys Ile Glu Gly Glu  
200 205 210



atc ctt ttc gac gga aag aac ctc ctt gat ctg aaa cca gac gag ctc Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu Lys Pro Asp Glu Leu 215 220 225	787
aat gca ctg cgt gga cat gaa atc gcc atg atc tac caa gat gca ctc Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile Tyr Gln Asp Ala Leu 230 235 240 245	835
tcc tca ctc aac cca tcc atg ctg atc agc gcc caa atg aag cag ctg Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala Gln Met Lys Gln Leu 250 255 260	883
acc cgc cgc ggt gga aag cgc agt gcc gaa gaa ctc ctg gaa ctt gta Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu Leu Leu Glu Leu Val 265 270 275	931
ggc ctt gat cca aag cgc acc ctg cag tcc tac ccg cat gag ctt tca Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr Pro His Glu Leu Ser 280 285 290	979
ggt ggc cag cgc cag cga gtt ctc atc gca atg gca ctg acc aga aac Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met Ala Leu Thr Arg Asn 295 300 305	1027
cca cgc ctc ctc atc gcc gac gag cca acc acc gcg cta gac gtc act Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr 310 315 320 325	1075
gtt cag cag cag gtt gtc gat ctg ctt aat gaa ctg cgt gaa aag ctc Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu Leu Arg Glu Lys Leu 330 335 340	1123
gga ttc gcc atg atc ttt gta tcc cac gac ttg gct ctt gtc gcc cgc Gly Phe Ala Met Ile Phe Val Ser His Asp Leu Ala Leu Val Ala Arg 345 350 355	1171
ctg gtg cac aag ctc acc gtc atg tac gca ggt cag gtt gtt gag caa Leu Val His Lys Leu Thr Val Met Tyr Ala Gly Gln Val Val Glu Gln 360 365 370	1219
gga acc acc cgc gaa atc ctt atc gat cct cga cac gaa tac acc cgc Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg His Glu Tyr Thr Arg 375 380 385	1267
ggt ttg ctc gga tcc gtg ctc tcc atc gaa gct ggt gtg gac cgc ctc Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala Gly Val Asp Arg Leu 390 395 400 405	1315
tac cag gtc cca ggc act gtt cca tca cca aag gaa ttc gtg gca ggc Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys Glu Phe Val Ala Gly 410 415 420	1363
gac cgc ttt gca cca cga tca gaa ttc cca gaa ctt ggc ctt gac caa Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu Leu Gly Leu Asp Gln 425 430 435	1411
aag cca gta ctt cgc ccc atc acg ggc aca gag cat gca tac gca gca Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu His Ala Tyr Ala Ala 440 445 450	1459

acc gat gaa ctt ctt gcc gca aag gga gaa caa cga tgacctcgac 1505  
 Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln Arg  
 455 460 465

aatcgacacc agg 1518

<210> 284  
 <211> 465  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 284  
 Met Ala Pro Ile Leu Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile  
 1 5 10 15  
 Val Phe Glu Ala Ser Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro  
 20 25 30  
 Ser Pro Ser Trp Gly Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu  
 35 40 45  
 Ser Gly Ala Trp Trp Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu  
 50 55 60  
 Thr Val Leu Cys Leu Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu  
 65 70 75 80  
 Ala Ser Pro Lys Pro Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu  
 85 90 95  
 Lys Lys Glu Glu Ser Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly  
 100 105 110  
 His Thr Thr Arg Glu Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala  
 115 120 125  
 Ala Leu Ser Thr Ser Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp  
 130 135 140  
 Gly Asn Pro Thr Pro Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe  
 145 150 155 160  
 Pro Asn Ala His Gly Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr  
 165 170 175  
 Val Ala Pro Gly Gln Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly  
 180 185 190  
 Lys Ser Ile Thr Ala Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala  
 195 200 205  
 Lys Ile Glu Gly Glu Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu  
 210 215 220  
 Lys Pro Asp Glu Leu Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile  
 225 230 235 240  
 Tyr Gln Asp Ala Leu Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala  
 245 250 255

Gln Met Lys Gln Leu Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu  
 260 265 270  
 Leu Leu Glu Leu Val Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr  
 275 280 285  
 Pro His Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met  
 290 295 300  
 Ala Leu Thr Arg Asn Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr  
 305 310 315 320  
 Ala Leu Asp Val Thr Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu  
 325 330 335  
 Leu Arg Glu Lys Leu Gly Phe Ala Met Ile Phe Val Ser His Asp Leu  
 340 345 350  
 Ala Leu Val Ala Arg Leu Val His Lys Leu Thr Val Met Tyr Ala Gly  
 355 360 365  
 Gln Val Val Glu Gln Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg  
 370 375 380  
 His Glu Tyr Thr Arg Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala  
 385 390 395 400  
 Gly Val Asp Arg Leu Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys  
 405 410 415  
 Glu Phe Val Ala Gly Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu  
 420 425 430  
 Leu Gly Leu Asp Gln Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu  
 435 440 445  
 His Ala Tyr Ala Ala Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln  
 450 455 460  
 Arg  
 465

<210> 285  
 <211> 783  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(760)  
 <223> RXA02664

<400> 285  
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 catcaacttc aaggcctacc gcgatgaagt aatcggcata gtg ggt gaa tct ggt 115  
 Val Gly Glu Ser Gly  
 1 5  
 tgc gga aaa tct acc ctt gcc cgc gtt atg gtt ggc ctg caa ccg gtc 163

Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val Gly Leu Gln Pro Val	
10 15 20	
acc tcc ggc gaa gtg ctg ttc aaa ggc aag ccc atg aag cct cgt ggt	211
Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro Met Lys Pro Arg Gly	
25 30 35	
gcg cag cgc aaa gaa ctc ggc agc tca gta tcc gtc gtg ttc cag gat	259
Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser Val Val Phe Gln Asp	
40 45 50	
cct gcc acc tcg tta aac cca cga atg acc gtg cgc gaa cag ctc ctc	307
Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val Arg Glu Gln Leu Leu	
55 60 65	
gat cca ctt cga gta cac aaa gtt ggc gat gaa gca tcc cgc aac cag	355
Asp Pro Leu Arg Val His Lys Val Gly Asp Glu Ala Ser Arg Asn Gln	
70 75 80 85	
tgg gtt tca gag ctg atc tcc atg gtt ggc ctc ccg caa tcc gcg ttg	403
Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu Pro Gln Ser Ala Leu	
90 95 100	
gaa gta ctc ccc cga cag gtt tcc ggt ggc caa cgc caa cgc gtg gcc	451
Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln Arg Gln Arg Val Ala	
105 110 115	
att gct cga gca ctt gcg ctg aaa cct gac atc atc gtt gcc gac gaa	499
Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile Ile Val Ala Asp Glu	
120 125 130	
cca acc tcc gcg ctg gat gta tcc gtt cgt gcg cag gtc ctc aac ctt	547
Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala Gln Val Leu Asn Leu	
135 140 145	
ctg ctg gat ctg aaa act gaa ctc ggc ctg gga ttg gta ttc atc tcc	595
Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly Leu Val Phe Ile Ser	
150 155 160 165	
cac gac atc aac act gtt cgc tac gtt tct gat cgc atc gca gtc atg	643
His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp Arg Ile Ala Val Met	
170 175 180	
ctg gct gga gaa atc att gag gaa aac acc acc tca gag atc ttc aac	691
Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr Ser Glu Ile Phe Asn	
185 190 195	
aat gcg cag cag gac tac acc cgc act ctg ctc gaa gcg aca cca tcg	739
Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu Glu Ala Thr Pro Ser	
200 205 210	
ctg ctg aac aaa act cgt ttg tagtctccaa ccctttattc cct	783
Leu Leu Asn Lys Thr Arg Leu	
215 220	

&lt;210&gt; 286

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 286

Val Gly Glu Ser Gly Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val  
 1 5 10 15  
 Gly Leu Gln Pro Val Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro  
 20 25 30  
 Met Lys Pro Arg Gly Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser  
 35 40 45  
 Val Val Phe Gln Asp Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val  
 50 55 60  
 Arg Glu Gln Leu Leu Asp Pro Leu Arg Val His Lys Val Gly Asp Glu  
 65 70 75 80  
 Ala Ser Arg Asn Gln Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu  
 85 90 95  
 Pro Gln Ser Ala Leu Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln  
 100 105 110  
 Arg Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile  
 115 120 125  
 Ile Val Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala  
 130 135 140  
 Gln Val Leu Asn Leu Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly  
 145 150 155 160  
 Leu Val Phe Ile Ser His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp  
 165 170 175  
 Arg Ile Ala Val Met Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr  
 180 185 190  
 Ser Glu Ile Phe Asn Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu  
 195 200 205  
 Glu Ala Thr Pro Ser Leu Leu Asn Lys Thr Arg Leu  
 210 215 220

&lt;210&gt; 287

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1132)

&lt;223&gt; RXA00760

&lt;400&gt; 287

accacggttg tctccattgt cactgtgctg gtcacgtct acatcatcgc caaccttctc 60

gtggacttga tctacgccgt tctcgatccg aggatccgct atg cct aat aat gaa 115  
 Met Pro Asn Asn Glu  
 1 5

ttc cac aca aac cac tcg ttg ggc caa gat gat caa acc cca gat cag	163
Phe His Thr Asn His Ser Leu Gly Gln Asp Asp Gln Thr Pro Asp Gln	
10 15 20	
gct cat ttc ttc cca caa gga cga ggc gag gct cta gtt cga cca ggt	211
Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala Leu Val Arg Pro Gly	
25 30 35	
caa gag cac ttc atc gca gcc act gat gaa acc gga ctt ggt gcc gtc	259
Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr Gly Leu Gly Ala Val	
40 45 50	
gat gct gtt gct gat gac tct gca cca acc tcc atg tgg ggc gaa gcg	307
Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser Met Trp Gly Glu Ala	
55 60 65	
tgg cga gac ctt cgt cgt cga cca ctg ttc tgg gtc tct gcg gtg ttg	355
Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp Val Ser Ala Val Leu	
70 75 80 85	
att att ttg gcg ctt ctc ctg gcc gca gtt ccg cag ctg ttt acc tca	403
Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro Gln Leu Phe Thr Ser	
90 95 100	
acg gat ccc cag ttc tgt gtg ctg gca aac tct ctt gat ggt cca cag	451
Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser Leu Asp Gly Pro Gln	
105 110 115	
tct gga cat ccc ttc gga ttc gac cgt caa ggt tgc gat att ttt gct	499
Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly Cys Asp Ile Phe Ala	
120 125 130	
cgt acc gtc tac ggt gct cgt gcc tcg gtc gcc gtc ggt gtg ttg acc	547
Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala Val Gly Val Leu Thr	
135 140 145	
acg tta ctg gtc gcc ctc atc ggt act gta ttt ggt gct ttg gct ggc	595
Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe Gly Ala Leu Ala Gly	
150 155 160 165	
ttc ttt ggt ggc atc atg gat acc atc ctc tcc cgc atc acc gac atg	643
Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser Arg Ile Thr Asp Met	
170 175 180	
ttc ttc gcc att cca ctg gtt ctg gca gcc atc gtt gtg atg cag atg	691
Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile Val Val Met Gln Met	
185 190 195	
ttc aag gaa cac cgc acc atc gtc acc gtg gtt ttg gtg ctt ggg ctt	739
Phe Lys Glu His Arg Thr Ile Val Thr Val Val Leu Val Leu Gly Leu	
200 205 210	
ttc ggc tgg acc aac att gcg cgt att acc cgt gga gcg gtg atg acc	787
Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg Gly Ala Val Met Thr	
215 220 225	
gca aag aat gaa gag tat gtc acc tcc gca cgt gcg ctt ggt gca tca	835
Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg Ala Leu Gly Ala Ser	
230 235 240 245	
aaa gcc aag ata ctg ctg tct cac atc atg cca aac gcc gca gca ccc	883

Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro Asn Ala Ala Ala Pro  
 250 255 260  
 atc att gtg tat gca act gtg gca ctg gga aca ttc atc gtg gca gag 931  
 Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr Phe Ile Val Ala Glu  
 265 270 275  
 gcg acg ctc tcc ttc ctg ggc att ggc ctt cca cca tca att gtc tcc 979  
 Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro Pro Ser Ile Val Ser  
 280 285 290  
 tgg ggt gct gat atc gcg aag gca caa acc tcc ctt cgt acc caa ccc 1027  
 Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser Leu Arg Thr Gln Pro  
 295 300 305  
 atg gtg ctg ttc tac ccc gca atg gca ctt gca cta acc gtt ttg agc 1075  
 Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala Leu Thr Val Leu Ser  
 310 315 320 325  
 ttc atc atg atg ggc gat gtc gtc cgc gac gct ctg gat cct aag tcg 1123  
 Phe Ile Met Met Gly Asp Val Val Arg Asp Ala Leu Asp Pro Lys Ser  
 330 335 340  
 agg aag cga tgaccaccaa catcccacaa acc 1155  
 Arg Lys Arg

&lt;210&gt; 288

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 288

Met Pro Asn Asn Glu Phe His Thr Asn His Ser Leu Gly Gln Asp Asp  
 1 5 10 15  
 Gln Thr Pro Asp Gln Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala  
 20 25 30  
 Leu Val Arg Pro Gly Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr  
 35 40 45  
 Gly Leu Gly Ala Val Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser  
 50 55 60  
 Met Trp Gly Glu Ala Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp  
 65 70 75 80  
 Val Ser Ala Val Leu Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro  
 85 90 95  
 Gln Leu Phe Thr Ser Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser  
 100 105 110  
 Leu Asp Gly Pro Gln Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly  
 115 120 125  
 Cys Asp Ile Phe Ala Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala  
 130 135 140

Val Gly Val Leu Thr Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe  
145 150 155 160

Gly Ala Leu Ala Gly Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser  
165 170 175

Arg Ile Thr Asp Met Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile  
180 185 190

Val Val Met Gln Met Phe Lys Glu His Arg Thr Ile Val Thr Val Val  
195 200 205

Leu Val Leu Gly Leu Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg  
210 215 220

Gly Ala Val Met Thr Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg  
225 230 235 240

Ala Leu Gly Ala Ser Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro  
245 250 255

Asn Ala Ala Ala Pro Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr  
260 265 270

Phe Ile Val Ala Glu Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro  
275 280 285

Pro Ser Ile Val Ser Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser  
290 295 300

Leu Arg Thr Gln Pro Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala  
305 310 315 320

Leu Thr Val Leu Ser Phe Ile Met Met Gly Asp Val Val Arg Asp Ala  
325 330 335

Leu Asp Pro Lys Ser Arg Lys Arg  
340

<210> 289

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXA02035

<400> 289

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catttagttt cccggatcac accgactaat ctcagaagcc atg aag atc acg cgc 115  
Met Lys Ile Thr Arg  
1 5

gga ctc ctg cca tca ttg ctg ttg gca agc aca atc gtg gtg tcg tca 163  
Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr Ile Val Val Ser Ser  
10 15 20



tgc tct gct gga tgc act gcg tat cag cag ccc cct gct gtt gat caa	211
Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro Pro Ala Val Asp Gln	
25 30 35	
tca tcc att gtc att gct acc acg gct gct gcg gcg tca ctt gat ttc	259
Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala Ala Ser Leu Asp Phe	
40 45 50	
acc aat gct gcg ggc gct gct att ccg cag gcg atg atg tcc aat att	307
Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala Met Met Ser Asn Ile	
55 60 65	
tac gag ggg ctt gtg cgc atc gat gcg gag ggt gag att cag ccg ctg	355
Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly Glu Ile Gln Pro Leu	
70 75 80 85	
ctt gcc acg tgc tgg gat att tca gac gat cgc acc gag tac att ttc	403
Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg Thr Glu Tyr Ile Phe	
90 95 100	
cat ttg cgg gag ggt gtg ctg ttt tcc aac ggc gat ccc ttc aat gct	451
His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly Asp Pro Phe Asn Ala	
105 110 115	
gat tct gcg aag ttt tcc att gat cgg gta aaa act gac tgg acc aat	499
Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys Thr Asp Trp Thr Asn	
120 125 130	
ggt ttg aaa agt ggc atg gat gtg gtg gag tcc acc gag gtg att gac	547
Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser Thr Glu Val Ile Asp	
135 140 145	
gat cac acg ctg aaa gtt tgc ctg gtc agg ccg tcc aac caa tgg ttg	595
Asp His Thr Leu Lys Val Ser Leu Val Arg Pro Ser Asn Gln Trp Leu	
150 155 160 165	
tgg agc atg ggt acc gcg atc ggt gcc atg atg acg gag ggg ggc gtc	643
Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met Thr Glu Gly Gly Val	
170 175 180	
gat aag ctg gca act gat ccc gtt ggc acc ggc ccg tac acg gtg acg	691
Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly Pro Tyr Thr Val Thr	
185 190 195	
cac tgg gcg ccg ggc cgc gca att ggg ttc ggc gcg ccg gcc gat tat	739
His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly Ala Arg Ala Asp Tyr	
200 205 210	
tgg ggg cag aag ccg ctt aac gac gcc gca acc atc cgc tac ttc agc	787
Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr Ile Arg Tyr Phe Ser	
215 220 225	
gat gcg acg gcc tgc acc aat gcg ctg caa agc ggt gac gtg gac gtg	835
Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser Gly Asp Val Asp Val	
230 235 240 245	
att tgg gcg atg caa gcg ccc gaa cag ctg gct acg ctg cag gaa tac	883
Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala Thr Leu Gln Glu Tyr	
250 255 260	
acc gtg gaa gtg ggc aca acc aat ggt gag atg ttg ctg tgc atg aat	931

Thr	Val	Glu	Val	Gly	Thr	Thr	Asn	Gly	Glu	Met	Leu	Leu	Ser	Met	Asn	
			265				270				275					
aat	cag	cgt	gca	cct	ttt	gat	gat	gtg	cgt	gtg	cgc	cag	gcg	gtg	atg	979
Asn	Gln	Arg	Ala	Pro	Phe	Asp	Asp	Val	Arg	Val	Arg	Gln	Ala	Val	Met	
			280				285				290					
ttt	gcg	att	gat	cgc	caa	gcc	gtc	att	gat	acc	gcg	ttg	gaa	ggg	tac	1027
Phe	Ala	Ile	Asp	Arg	Gln	Ala	Val	Ile	Asp	Thr	Ala	Leu	Glu	Gly	Tyr	
			295				300				305					
ggc	acc	gac	act	ggg	ggc	gtg	cct	gtt	ccg	ccg	act	gat	ccg	tgg	tac	1075
Gly	Thr	Asp	Thr	Gly	Gly	Val	Pro	Val	Pro	Pro	Thr	Asp	Pro	Trp	Tyr	
			310				315				320				325	
gag	aaa	tcc	acg	atg	tac	ccc	tac	gat	ccg	gac	cgc	gca	cgg	gca	ttg	1123
Glu	Lys	Ser	Thr	Met	Tyr	Pro	Tyr	Asp	Pro	Asp	Arg	Ala	Arg	Ala	Leu	
			330				335				340					
tta	gag	gag	gcc	ggc	gcc	gag	gga	acg	cgg	atc	acc	atg	tcc	att	cct	1171
Leu	Glu	Glu	Ala	Gly	Ala	Glu	Gly	Thr	Arg	Ile	Thr	Met	Ser	Ile	Pro	
			345				350				355					
tcg	ttg	ccg	tac	gct	cag	gca	gcc	tct	gaa	atc	ctg	tac	tcg	caa	ctg	1219
Ser	Leu	Pro	Tyr	Ala	Gln	Ala	Ala	Ser	Glu	Ile	Leu	Tyr	Ser	Gln	Leu	
			360				365				370					
cga	gat	gtt	ggg	ttt	gat	cct	gtg	att	gaa	tca	acc	gag	ttc	cca	gcc	1267
Arg	Asp	Val	Gly	Phe	Asp	Pro	Val	Ile	Glu	Ser	Thr	Glu	Phe	Pro	Ala	
			375				380				385					
gtc	tgg	ttg	gca	cag	gtc	atg	ggg	caa	aaa	gac	tac	gac	atg	tca	cta	1315
Val	Trp	Leu	Ala	Gln	Val	Met	Gly	Gln	Lys	Asp	Tyr	Asp	Met	Ser	Leu	
			390				395				400				405	
atc	gcg	cat	gtg	gaa	ccc	cgc	gac	atc	ccc	acg	ctg	ttt	agc	ccc	aac	1363
Ile	Ala	His	Val	Glu	Pro	Arg	Asp	Ile	Pro	Thr	Leu	Phe	Ser	Pro	Asn	
			410				415				420					
tac	tat	ttg	ggc	ttt	gac	gac	acc	gaa	acc	caa	gcc	ctc	ctc	gca	gag	1411
Tyr	Tyr	Leu	Gly	Phe	Asp	Asp	Thr	Glu	Thr	Gln	Ala	Leu	Leu	Ala	Glu	
			425				430				435					
gca	gac	agt	tca	gca	aac	gaa	gtg	gaa	ttg	atg	caa	caa	gct	gtc	gat	1459
Ala	Asp	Ser	Ser	Ala	Asn	Glu	Val	Glu	Leu	Met	Gln	Gln	Ala	Val	Asp	
			440				445				450					
cga	atc	atg	gaa	caa	gcc	gtc	gcc	gac	aac	ctc	atg	aac	gtg	gcc	aac	1507
Arg	Ile	Met	Glu	Gln	Ala	Val	Ala	Asp	Asn	Leu	Met	Asn	Val	Ala	Asn	
			455				460				465					
atc	gtg	gtg	atg	tca	cca	gag	atc	acc	ggc	att	gat	ccc	aac	gtg	gtg	1555
Ile	Val	Val	Met	Ser	Pro	Glu	Ile	Thr	Gly	Ile	Asp	Pro	Asn	Val	Val	
			470				475				480				485	
tcc	ggg	gcg	ttg	gaa	ttg	tcg	ttg	att	ggg	cgg	aaa	gaa	tcc	ggg	gta	1603
Ser	Gly</															

&lt;210&gt; 290

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 290

Met	Lys	Ile	Thr	Arg	Gly	Leu	Leu	Pro	Ser	Leu	Leu	Leu	Ala	Ser	Thr
1				5					10					15	
Ile	Val	Val	Ser	Ser	Cys	Ser	Ala	Gly	Ser	Thr	Ala	Tyr	Gln	Gln	Pro
			20					25					30		
Pro	Ala	Val	Asp	Gln	Ser	Ser	Ile	Val	Ile	Ala	Thr	Thr	Ala	Ala	Ala
			35				40					45			
Ala	Ser	Leu	Asp	Phe	Thr	Asn	Ala	Ala	Gly	Ala	Ala	Ile	Pro	Gln	Ala
	50					55					60				
Met	Met	Ser	Asn	Ile	Tyr	Glu	Gly	Leu	Val	Arg	Ile	Asp	Ala	Glu	Gly
65					70					75				80	
Glu	Ile	Gln	Pro	Leu	Leu	Ala	Thr	Ser	Trp	Asp	Ile	Ser	Asp	Asp	Arg
				85					90					95	
Thr	Glu	Tyr	Ile	Phe	His	Leu	Arg	Glu	Gly	Val	Leu	Phe	Ser	Asn	Gly
			100					105						110	
Asp	Pro	Phe	Asn	Ala	Asp	Ser	Ala	Lys	Phe	Ser	Ile	Asp	Arg	Val	Lys
		115					120					125			
Thr	Asp	Trp	Thr	Asn	Gly	Leu	Lys	Ser	Gly	Met	Asp	Val	Val	Glu	Ser
	130					135					140				
Thr	Glu	Val	Ile	Asp	Asp	His	Thr	Leu	Lys	Val	Ser	Leu	Val	Arg	Pro
145					150					155					160
Ser	Asn	Gln	Trp	Leu	Trp	Ser	Met	Gly	Thr	Ala	Ile	Gly	Ala	Met	Met
				165					170					175	
Thr	Glu	Gly	Gly	Val	Asp	Lys	Leu	Ala	Thr	Asp	Pro	Val	Gly	Thr	Gly
			180					185					190		
Pro	Tyr	Thr	Val	Thr	His	Trp	Ala	Pro	Gly	Arg	Ala	Ile	Gly	Phe	Gly
			195				200						205		
Ala	Arg	Ala	Asp	Tyr	Trp	Gly	Gln	Lys	Pro	Leu	Asn	Asp	Ala	Ala	Thr
	210					215					220				
Ile	Arg	Tyr	Phe	Ser	Asp	Ala	Thr	Ala	Ser	Thr	Asn	Ala	Leu	Gln	Ser
225					230					235					240
Gly	Asp	Val	Asp	Val	Ile	Trp	Ala	Met	Gln	Ala	Pro	Glu	Gln	Leu	Ala
				245					250					255	
Thr	Leu	Gln	Glu	Tyr	Thr	Val	Glu	Val	Gly	Thr	Thr	Asn	Gly	Glu	Met
			260					265					270		
Leu	Leu	Ser	Met	Asn	Asn	Gln	Arg	Ala	Pro	Phe	Asp	Asp	Val	Arg	Val

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<400> 291
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caactaattt ccctgtttcc aataactcaag gtgtgcgcat atg aat tct gat gct 115
               Met Asn Ser Asp Ala
               1           5

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tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg	163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val	
10 15 20	
acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc	211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile	
25 30 35	
aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa	259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys	
40 45 50	
tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc	307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly	
55 60 65	
acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca	355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala	
70 75 80 85	
ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac	403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn	
90 95 100	
ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc	451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe	
105 110 115	
gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac	499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His	
120 125 130	
gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac	547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His	
135 140 145	
aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc	595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg	
150 155 160 165	
gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca	643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala	
170 175 180	
gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg	691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met	
185 190 195	
cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg	739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val	
200 205 210	
aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg	787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val	
215 220 225	
ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc	835
Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala	
230 235 240 245	

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883  
 Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys  
                   250                                  255                                  260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927  
 Asp Leu Leu Gly Asp Arg Ala  
                   265

<210> 292

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe  
   1                                  5                                  10                                  15

Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp  
                   20                                  25                                  30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu  
                   35                                  40                                  45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val  
                   50                                  55                                  60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr  
   65                                  70                                  75                                  80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile  
                                   85                                  90                                  95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val  
                   100                                  105                                  110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly  
                   115                                  120                                  125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser  
   130                                  135                                  140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly  
  145                                  150                                  155                                  160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro  
                                   165                                  170                                  175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr  
                   180                                  185                                  190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly  
                   195                                  200                                  205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr  
   210                                  215                                  220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly  
  225                                  230                                  235                                  240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg

245

250

255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala  
 260 265

&lt;210&gt; 293

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

&lt;223&gt; FRXA01002

&lt;400&gt; 293

ccc acg gag cac gac aag cag att gct ttt cac gcg ttg gag tcc gtg 48  
 Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val  
 1 5 10 15

ggc att ttg gac aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga 96  
 Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly  
 20 25 30

cag aaa cag cgc gtt gct att gcg cgc gcc tta tcg caa gat ccg tct 144  
 Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser  
 35 40 45

gtc atg ctg gca gat gag cct gtg gca agc ctt gat ccg cca acc gcg 192  
 Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala  
 50 55 60

cat tcc gtg atg cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc 240  
 His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu  
 65 70 75 80

acc gtg ttg gtg aac ttg cac ttg att gat ttg gct cgt caa tac acc 288  
 Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr  
 85 90 95

aca agg ctt gtg ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct 336  
 Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro  
 100 105 110

atc tct gag gcc acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc 384  
 Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro  
 115 120 125

atc cag gct aaa gac ctg cta ggt gat cgc gca tgaccacgcc ttctttctaca 437  
 Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala  
 130 135

ctt 440

&lt;210&gt; 294

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val  
 1 5 10 15

Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly  
 20 25 30

Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser  
 35 40 45

Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala  
 50 55 60

His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu  
 65 70 75 80

Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr  
 85 90 95

Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro  
 100 105 110

Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro  
 115 120 125

Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala  
 130 135

&lt;210&gt; 295

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(946)

&lt;223&gt; RXN01000

&lt;400&gt; 295

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tcattgaagt aatctccaac gcaacttcgaa agaggctggg atg agc acc tta acc 115  
 Met Ser Thr Leu Thr  
 1 5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163  
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn  
 10 15 20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211  
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu  
 25 30 35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259  
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met  
 40 45 50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307  
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp  
 55 60 65



tgg tgc aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc	355
Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala	
70 75 80 85	
atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg	403
Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu	
90 95 100	
gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt	451
Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val	
105 110 115	
tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc	499
Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile	
120 125 130	
gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg	547
Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala	
135 140 145	
ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat	595
Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr	
150 155 160 165	
gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca	643
Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala	
170 175 180	
gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag	691
Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln	
185 190 195	
gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac	739
Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn	
200 205 210	
atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt	787
Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly	
215 220 225	
agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc	835
Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly	
230 235 240 245	
atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc	883
Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile	
250 255 260	
tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc	931
Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val	
265 270 275	
gtg gca cca agc aac tgacgctcca ccaagcatcc gca	969
Val Ala Pro Ser Asn	
280	

&lt;210&gt; 296

&lt;211&gt; 282

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 296

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Pro	Ala	Arg	Pro	Asn	Lys	Leu	Ala	Arg	Asn	Ile	Val	Ala	Ile	Val	Ala
			20					25					30		
Ala	Leu	Ile	Val	Leu	Ile	Ala	Thr	Gly	Thr	Leu	Lys	Ile	Glu	Trp	Asn
		35					40					45			
Glu	Leu	Pro	Gln	Met	Pro	Ala	Gln	Val	Trp	His	Tyr	Leu	Glu	Leu	Met
	50					55					60				
Phe	Ser	Asp	Pro	Asp	Trp	Ser	Lys	Phe	Gly	Arg	Ala	Val	Gln	Glu	Met
	65				70					75					80
Trp	Arg	Ser	Ile	Ala	Met	Ala	Trp	Leu	Gly	Ala	Ile	Leu	Cys	Val	Val
				85					90					95	
Val	Ser	Val	Pro	Leu	Gly	Met	Leu	Ala	Ala	Arg	Gly	Val	Gly	Pro	Tyr
			100					105					110		
Trp	Leu	Arg	Thr	Val	Leu	Arg	Phe	Val	Phe	Ala	Val	Ile	Arg	Ala	Phe
		115					120						125		
Pro	Glu	Val	Val	Ile	Ala	Ile	Ile	Leu	Leu	Thr	Val	Thr	Gly	Leu	Thr
	130					135					140				
Pro	Phe	Thr	Gly	Ala	Leu	Ala	Leu	Gly	Ile	Ser	Gly	Ile	Gly	Gln	Gln
145					150					155					160
Ala	Lys	Trp	Thr	Tyr	Glu	Ala	Ile	Glu	Ser	Thr	Pro	Thr	Gly	Pro	Ser
				165					170					175	
Glu	Ala	Val	Arg	Ala	Ala	Gly	Gly	Thr	Thr	Pro	Glu	Val	Leu	Arg	Trp
			180					185					190		
Ala	Leu	Trp	Pro	Gln	Val	Ala	Pro	Ser	Ile	Ala	Ser	Phe	Ala	Leu	Tyr
		195					200					205			
Arg	Phe	Glu	Ile	Asn	Ile	Arg	Thr	Ser	Ala	Val	Leu	Gly	Ile	Val	Gly
	210					215					220				
Ala	Gly	Gly	Ile	Gly	Ser	Met	Leu	Ala	Asn	Tyr	Thr	Asn	Tyr	Arg	Gln
225					230					235					240
Trp	Asp	Thr	Val	Gly	Met	Leu	Leu	Ile	Val	Val	Val	Val	Ala	Thr	Met
				245					250					255	
Ile	Val	Asp	Leu	Ile	Ser	Gly	Thr	Ile	Arg	Arg	Arg	Ile	Met	Lys	Gly
			260					265					270		
Ala	Ser	Asp	Arg	Val	Val	Ala	Pro	Ser	Asn						
		275					280								

<210> 297

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA01000

<400> 297

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Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu	
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cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc gca	96
Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala	
20 25 30	
att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg ctc	144
Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu	
35 40 45	
gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat gaa	192
Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu	
50 55 60	
gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca gcg	240
Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala	
65 70 75 80	
ggt gga act acg ccg gag gtt ctg cgg tgg gcg ttg tgg cca cag gtt	288
Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val	
85 90 95	
gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac atc	336
Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile	
100 105 110	
cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt agt	384
Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser	
115 120 125	
atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc atg	432
Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met	
130 135 140	
ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc tcc	480
Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser	
145 150 155 160	
ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc gtg	528
Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val	
165 170 175	
gca cca agc aac tgacgctcca ccaagcatcc gca	563
Ala Pro Ser Asn	
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<210> 298

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

&lt;400&gt; 298

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 20 25 30

Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu  
 35 40 45

Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu  
 50 55 60

Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala  
 65 70 75 80

Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val  
 85 90 95

Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile  
 100 105 110

Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser  
 115 120 125

Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met  
 130 135 140

Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser  
 145 150 155 160

Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val  
 165 170 175

Ala Pro Ser Asn  
 180

&lt;210&gt; 299

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(904)

&lt;223&gt; RXA01003

&lt;400&gt; 299

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gtcgcccat ccaggctaaa gacctgctag gtgatcgcg atg acc acg cct tct 115  
 Met Thr Thr Pro Ser  
 1 5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc 163  
 Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu  
 10 15 20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg 211

Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala	
25 30 35	
cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc	259
Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg	
40 45 50	
aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc	307
Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe	
55 60 65	
ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt	355
Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu	
70 75 80 85	
gtt gga gct gtc ttg tct gct gcc gta tct gtg cct ttg acg ttg tgg	403
Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp	
90 95 100	
gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc	451
Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg	
105 110 115	
acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc	499
Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr	
120 125 130	
atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg	547
Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr	
135 140 145	
ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc	595
Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala	
150 155 160 165	
att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt	643
Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly	
170 175 180	
gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg	691
Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met	
185 190 195	
ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc	739
Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg	
200 205 210	
atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg	787
Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu	
215 220 225	
ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc	835
Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile	
230 235 240 245	
att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac	883
Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn	
250 255 260	
gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc	927
Ala Leu Arg Lys Arg Leu Val	

265

<210> 300  
 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 300

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			20					25					30		
Thr	Ala	Thr	Pro	Ala	Leu	Gly	Gly	Ile	Glu	Leu	Asp	Phe	Ala	Ser	Ile
			35				40					45			
Ala	Ala	Asn	Trp	Arg	Asn	Gly	Ala	Asn	Lys	Leu	Leu	Gln	Met	Leu	Gln
	50					55					60				
Pro	Asn	Phe	Ala	Phe	Leu	Pro	Arg	Thr	Trp	Leu	Pro	Met	Leu	Glu	Thr
65					70					75				80	
Leu	Gln	Met	Ala	Leu	Val	Gly	Ala	Val	Leu	Ser	Ala	Ala	Val	Ser	Val
				85					90					95	
Pro	Leu	Thr	Leu	Trp	Ala	Ala	Gln	Ala	Thr	Asn	Thr	Ser	Ala	Ile	Gly
			100					105					110		
Arg	Gly	Ile	Val	Arg	Thr	Ile	Ile	Asn	Val	Val	Arg	Ser	Val	Pro	Asp
		115					120					125			
Leu	Val	Tyr	Ala	Thr	Ile	Leu	Val	Ala	Met	Val	Gly	Val	Gly	Ala	Leu
	130					135					140				
Pro	Gly	Ile	Leu	Thr	Leu	Phe	Leu	Phe	Asn	Leu	Gly	Ile	Val	Val	Lys
145					150					155					160
Leu	Val	Ser	Glu	Ala	Ile	Asp	Ser	Thr	Glu	His	Pro	Tyr	Met	Glu	Ala
				165					170					175	
Gly	Arg	Ala	Ala	Gly	Gly	Ser	Gln	Phe	Gln	Ile	Asn	Arg	Val	Ser	Ala
			180					185					190		
Leu	Pro	Glu	Val	Met	Pro	Leu	Phe	Ala	Asn	Gln	Trp	Leu	Tyr	Thr	Leu
		195					200					205			
Glu	Leu	Asn	Val	Arg	Ile	Ser	Ala	Ile	Leu	Gly	Ile	Val	Gly	Ala	Gly
	210					215					220				
Gly	Ile	Gly	Arg	Leu	Leu	Asp	Glu	Arg	Arg	Ala	Phe	Tyr	Ala	Tyr	Ala
225				230						235					240
Asp	Val	Ser	Val	Ile	Ile	Leu	Glu	Ile	Leu	Ile	Val	Val	Ile	Val	Ile
				245					250					255	
Glu	Val	Ile	Ser	Asn	Ala	Leu	Arg	Lys	Arg	Leu	Val				
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<210> 301  
 <211> 594  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(594)  
 <223> RXN00193

<220>  
 <223> All occurrences of n = any nucleotide

<220>  
 <223> All occurrences of Xaa = any amino acid

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 1 5 10 15  
 gtc ctc gtg gtc atc gtc tcc gtg atc aca gtc aac atc ttc gcc ttc 96  
 Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe  
 20 25 30  
 ctc ttg gcg tgg ttg ctg acc cgc aaa ctc cgc ggt acc aac ttt ttc 144  
 Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe  
 35 40 45  
 cgc aca gtc ttc ttt atg ccg aac ctt atc ggc ggc att gtg ctg ggt 192  
 Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly  
 50 55 60  
 tat acc tgg cag acc atg atc aac gcc gtg ctt tcg cac tat gcc acg 240  
 Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr  
 65 70 75 80  
 act att agc gcg gac tgg aaa ttc ggc tac gcc ggc ctc atc atg cta 288  
 Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu  
 85 90 95  
 ctt aac tgg cag ctc atc ggc tac atg atg atc att tac atc gcc ggc 336  
 Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly  
 100 105 110  
 ctg caa aac gtc cca cca gag ctc att gag gct gcc gaa ctc gac ggc 384  
 Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly  
 115 120 125  
 gtc aac aag tgg gag atg ctg cgg cac gtc act att ccg atg gtc atg 432  
 Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met  
 130 135 140  
 cca tcc atc acc atc tgc ctc ttt ttg act ttg tcg aac tcc ttt aag 480  
 Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys  
 145 150 155 160  
 ctc ttc gac cag aac ctg gcg ctg acc aac ggc gct cct ggc ggg caa 528  
 Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln  
 165 170 175

act gag atg gtg gcg ctc aac atc atc aac acg ctg ttt aac cgt atg 576  
 Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met  
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aat gtc gag ggc gtc ggt 594  
 Asn Val Glu Gly Val Gly  
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<210> 302

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 302

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Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe  
                   20                                  25                                  30

Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe  
                   35                                  40                                  45

Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly  
           50                                  55                                  60

Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr  
           65                                  70                                  75                                  80

Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu  
                   85                                  90                                  95

Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly  
                   100                                  105                                  110

Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly  
                   115                                  120                                  125

Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met  
           130                                  135                                  140

Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys  
           145                                  150                                  155                                  160

Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln  
                   165                                  170                                  175

Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met  
                   180                                  185                                  190

Asn Val Glu Gly Val Gly  
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<210> 303

<211> 940

<212> DNA



<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (75)..(917)

<223> FRXA00193

<400> 303

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aaggtttcac cacc atg caa gca acg ctg aag aag tac ttc cca gtc ttt      110
      Met Gln Ala Thr Leu Lys Lys Tyr Phe Pro Val Phe
      1              5              10

gtc ttg ccc acc ctt ctg gca ttc atg att gcc ttc ttg gtg ccg ttc      158
Val Leu Pro Thr Leu Leu Ala Phe Met Ile Ala Phe Leu Val Pro Phe
      15              20              25

atc gtg ggt ttc ttc ctc tcc ttt acg aag ttc acc act atc acc aac      206
Ile Val Gly Phe Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn
      30              35              40

gcc aag tgg gtt ggc ata gac aac tac gtc aaa gct ttc tcc caa cgc      254
Ala Lys Trp Val Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg
      45              50              55              60

gaa ggt ttc atc tca gcc ttc ggt ttc acc gtc ctc gtg gtc atc gtc      302
Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val
      65              70              75

tcc gtg atc aca gtc aac atc ttc gcc ttc ctc ttg gcg tgg ttg ctg      350
Ser Val Ile Thr Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu
      80              85              90

acc cgc aaa ctc cgc ggt acc aac ttt ttc cgc aca gtc ttc ttt atg      398
Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met
      95              100              105

ccg aac ctt atc ggc ggc att gtg ctg ggt tat acc tgg cag acc atg      446
Pro Asn Leu Ile Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met
      110              115              120

atc aac gcc gtg ctt tgc cac tat gcc acg act att agc gcg gac tgg      494
Ile Asn Ala Val Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp
      125              130              135              140

aaa ttc ggc tac gcc ggc ctc atc atg cta ctt aac tgg cag ctc atc      542
Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile
      145              150              155

ggc tac atg atg atc att tac atc gcc ggc ctg caa aac gtc cca cca      590
Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro
      160              165              170

gag ctc att gag gct gcc gaa ctc gac ggc gtc aac aag tgg gag atg      638
Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly Val Asn Lys Trp Glu Met
      175              180              185

ctg cgg cac gtc act att ccg atg gtc atg cca tcc atc acc atc tgc      686
Leu Arg His Val Thr Ile Pro Met Val Met Pro Ser Ile Thr Ile Cys
      190              195              200

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ctc ttt ttg act ttg tgg aac tcc ttt aag ctc ttc gac cag aac ctg 734  
 Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu  
 205 210 215 220

gcg ctg acc aac ggc gct cct ggc ggg caa act gag atg gtg gcg ctc 782  
 Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln Thr Glu Met Val Ala Leu  
 225 230 235

aac atc atc aac acg ctg ttt aac cgt atg aat gtc gag ggc gtc ggt 830  
 Asn Ile Ile Asn Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly  
 240 245 250

cag gcc aag gcc gtt atc ttc gtc gtc gtt gtg gtc gtc atc gcg tac 878  
 Gln Ala Lys Ala Val Ile Phe Val Val Val Val Val Ile Ala Tyr  
 255 260 265

ttc cag ctg cgc gcg acc cgc tcc aag gaa atc gag gct taagttatga 927  
 Phe Gln Leu Arg Ala Thr Arg Ser Lys Glu Ile Glu Ala  
 270 275 280

ctaccagcac ttc 940

<210> 304

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 304

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Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn Ala Lys Trp Val  
 35 40 45

Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg Glu Gly Phe Ile  
 50 55 60

Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val Ser Val Ile Thr  
 65 70 75 80

Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu  
 85 90 95

Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met Pro Asn Leu Ile  
 100 105 110

Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met Ile Asn Ala Val  
 115 120 125

Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr  
 130 135 140

Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile Gly Tyr Met Met  
 145 150 155 160

Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro Glu Leu Ile Glu

165										170					175															
Ala	Ala	Glu	Leu	Asp	Gly	Val	Asn	Lys	Trp	Glu	Met	Leu	Arg	His	Val															
			180						185						190															
Thr	Ile	Pro	Met	Val	Met	Pro	Ser	Ile	Thr	Ile	Cys	Leu	Phe	Leu	Thr															
			195					200					205																	
Leu	Ser	Asn	Ser	Phe	Lys	Leu	Phe	Asp	Gln	Asn	Leu	Ala	Leu	Thr	Asn															
		210					215					220																		
Gly	Ala	Pro	Gly	Gly	Gln	Thr	Glu	Met	Val	Ala	Leu	Asn	Ile	Ile	Asn															
		225				230					235				240															
Thr	Leu	Phe	Asn	Arg	Met	Asn	Val	Glu	Gly	Val	Gly	Gln	Ala	Lys	Ala															
				245					250					255																
Val	Ile	Phe	Val	Val	Val	Val	Val	Val	Ile	Ala	Tyr	Phe	Gln	Leu	Arg															
			260					265					270																	
Ala	Thr	Arg	Ser	Lys	Glu	Ile	Glu	Ala																						
		275					280																							

&lt;210&gt; 305

&lt;211&gt; 1053

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1030)

&lt;223&gt; RXN01298

&lt;400&gt; 305

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								Val	Ser	Thr	Leu	Ile		
								1				5		

tct	gaa	ccc	gag	gtg	gat	aag	cta	cgt	aaa	cgt	gcc	aag	aga	tca	agg	163
Ser	Glu	Pro	Glu	Val	Asp	Lys	Leu	Arg	Lys	Arg	Ala	Lys	Arg	Ser	Arg	
			10					15					20			

cgg	aca	gaa	tgg	tgg	ctt	gcc	gcc	gca	ctt	ctt	gcc	cca	aac	ttg	ctt	211
Arg	Thr	Glu	Trp	Trp	Leu	Ala	Ala	Ala	Leu	Leu	Ala	Pro	Asn	Leu	Leu	
		25					30					35				

ctc	ttg	gcc	atc	ttt	acg	tat	cgg	cca	ctg	tta	gat	aac	ttc	cgg	ttg	259
Leu	Leu	Ala	Ile	Phe	Thr	Tyr	Arg	Pro	Leu	Leu	Asp	Asn	Phe	Arg	Leu	
		40					45					50				

tcc	ttt	ttc	aac	tgg	aac	att	tcc	tcg	ccc	aca	tca	acc	ttc	att	ggg	307
Ser	Phe	Phe	Asn	Trp	Asn	Ile	Ser	Ser	Pro	Thr	Ser	Thr	Phe	Ile	Gly	
	55					60					65					

ttt	gat	aac	tac	gtt	gag	ttc	ttc	act	cgt	agt	gac	act	ctc	caa	gtt	355
Phe	Asp	Asn	Tyr	Val	Glu	Phe	Phe	Thr	Arg	Ser	Asp	Thr	Leu	Gln	Val	
	70				75					80				85		

gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg	403
Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met	
90 95 100	
gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc	451
Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly	
105 110 115	
cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt	499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly	
120 125 130	
gct gcc att ggt gtt gct ttc cag ttc gtt ttt gac cct aat ttt ggt	547
Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe Asp Pro Asn Phe Gly	
135 140 145	
ttg gtt cag gac ttg ctg gga cgc atc ggc gtt gat tcg cca cag ttc	595
Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val Asp Ser Pro Gln Phe	
150 155 160 165	
tac caa aac cct aac tgg gca ttg ttc atg gtg acg ttc act ttc gtg	643
Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val Thr Phe Thr Phe Val	
170 175 180	
tgg aag aac ttg ggc tac tcc ttt gtt atc tac ctg gct gca ttg cag	691
Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala Leu Gln	
185 190 195	
ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc gcg agc	739
Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly Ala Ser	
200 205 210	
gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc cca acc	787
Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg Pro Thr	
215 220 225	
acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag gtc ttc	835
Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln Val Phe	
230 235 240 245	
gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac ggt acg	883
Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn Gly Thr	
250 255 260	
acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac tat cgc	931
Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn Tyr Arg	
265 270 275	
gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg ctg ctg	979
Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu Leu Leu	
280 285 290	
att atc act gtt atc cag gtt cga tac atg gat aag gag aac aag cag	1027
Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn Lys Gln	
295 300 305	
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Lys	
310	

<210> 306  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 306

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			20					25					30		
Ala	Pro	Asn	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Thr	Tyr	Arg	Pro	Leu	Leu
		35					40					45			
Asp	Asn	Phe	Arg	Leu	Ser	Phe	Phe	Asn	Trp	Asn	Ile	Ser	Ser	Pro	Thr
	50					55					60				
Ser	Thr	Phe	Ile	Gly	Phe	Asp	Asn	Tyr	Val	Glu	Phe	Phe	Thr	Arg	Ser
65					70					75					80
Asp	Thr	Leu	Gln	Val	Val	Leu	Asn	Thr	Val	Ile	Phe	Thr	Ala	Cys	Ala
				85					90					95	
Val	Ile	Gly	Ser	Met	Val	Leu	Gly	Leu	Leu	Leu	Ala	Met	Leu	Leu	Asp
			100					105					110		
Gln	Lys	Leu	Phe	Gly	Arg	Asn	Phe	Val	Arg	Ser	Met	Val	Phe	Ala	Pro
		115					120					125			
Phe	Val	Ile	Ser	Gly	Ala	Ala	Ile	Gly	Val	Ala	Phe	Gln	Phe	Val	Phe
	130					135					140				
Asp	Pro	Asn	Phe	Gly	Leu	Val	Gln	Asp	Leu	Leu	Gly	Arg	Ile	Gly	Val
145					150					155					160
Asp	Ser	Pro	Gln	Phe	Tyr	Gln	Asn	Pro	Asn	Trp	Ala	Leu	Phe	Met	Val
			165					170						175	
Thr	Phe	Thr	Phe	Val	Trp	Lys	Asn	Leu	Gly	Tyr	Ser	Phe	Val	Ile	Tyr
			180					185					190		
Leu	Ala	Ala	Leu	Gln	Gly	Leu	Asn	Lys	Asp	Leu	Ser	Glu	Ala	Ala	Pro
		195					200					205			
Val	Asp	Gly	Ala	Ser	Ala	Trp	Thr	Arg	Phe	Trp	Lys	Val	Thr	Leu	Pro
	210					215					220				
Gln	Leu	Arg	Pro	Thr	Thr	Phe	Phe	Leu	Ser	Ile	Thr	Val	Thr	Leu	Asn
225					230					235					240
Ser	Val	Gln	Val	Phe	Asp	Ile	Ile	His	Thr	Met	Thr	Arg	Gly	Gly	Pro
			245					250						255	
Leu	Gly	Asn	Gly	Thr	Thr	Thr	Leu	Val	Tyr	Gln	Val	Tyr	Thr	Glu	Thr
		260					265						270		
Phe	Thr	Asn	Tyr	Arg	Ala	Gly	Tyr	Gly	Ala	Thr	Ile	Ala	Thr	Ile	Leu
		275					280					285			
Phe	Leu	Leu	Leu	Leu	Ile	Ile	Thr	Val	Ile	Gln	Val	Arg	Tyr	Met	Asp

290

295

300

Lys Glu Asn Lys Gln Lys  
305 310

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<211> 416  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (1)..(393)  
<223> FRXA01298

<400> 307  
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1 5 10 15  
ttg cag ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc 96  
Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly  
20 25 30  
gcg agc gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc 144  
Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg  
35 40 45  
cca acc acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag 192  
Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln  
50 55 60  
gtc ttc gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac 240  
Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn  
65 70 75 80  
ggt acg acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac 288  
Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn  
85 90 95  
tat cgc gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg 336  
Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu  
100 105 110  
ctg ctg att atc act gtt atc cag gtt cga tac atg gat aag gag aac 384  
Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn  
115 120 125  
aag cag aaa tgatctcgac tgatagaaac gtt 416  
Lys Gln Lys  
130

<210> 308  
<211> 131  
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<400> 308  
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Ala Ser Ala	Trp Thr Arg Phe Trp Lys	Val Thr Leu Pro	Gln Leu Arg
	35	40	45
Pro Thr Thr	Phe Phe Leu Ser Ile Thr	Val Thr Leu Asn	Ser Val Gln
	50	55	60
Val Phe Asp	Ile Ile His Thr Met Thr	Arg Gly Gly Pro	Leu Gly Asn
	65	70	75
Gly Thr Thr	Thr Leu Val Tyr Gln Val	Tyr Thr Glu Thr	Phe Thr Asn
	85	90	95
Tyr Arg Ala	Gly Tyr Gly Ala Thr Ile	Ala Thr Ile Leu	Phe Leu Leu
	100	105	110
Leu Leu Ile	Ile Thr Val Ile Gln Val	Arg Tyr Met Asp	Lys Glu Asn
	115	120	125
Lys Gln Lys			
	130		

&lt;210&gt; 309

&lt;211&gt; 535

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; FRXA02422

&lt;400&gt; 309

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aacactaatc ggacatttag gtcacataac atttccgctc gtg tcc aca tta att 115
                               Val Ser Thr Leu Ile
                               1 5

tct gaa ccc gag gtg gat aag cta cgt aaa cgt gcc aag aga tca agg 163
Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg
                               10 15 20

cgg aca gaa tgg tgg ott gcc gcc gca ctt ctt gcc cca aac ttg ctt 211
Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu
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ctc ttg gcc atc ttt acg tat cgg cca ctg tta gat aac ttc cgg ttg 259
Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu
                               40 45 50

tcc ttt ttc aac tgg aac att tcc tcg ccc aca tca acc ttc att ggg 307
Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr Ser Thr Phe Ile Gly
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ttt gat aac tac gtt gag ttc ttc act cgt agt gac act ctc caa gtt 355

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 70 75 80 85  
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 Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met  
 90 95 100  
 gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc 451  
 Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly  
 105 110 115  
 cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt 499  
 Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly  
 120 125 130  
 gct gcc att ggt ggt gct ttc cag ttc gtt ttt gac 535  
 Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe Asp  
 135 140 145

&lt;210&gt; 310

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 310

Val Ser Thr Leu Ile Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg  
 1 5 10 15  
 Ala Lys Arg Ser Arg Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu  
 20 25 30  
 Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu  
 35 40 45  
 Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr  
 50 55 60  
 Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser  
 65 70 75 80  
 Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala  
 85 90 95  
 Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp  
 100 105 110  
 Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro  
 115 120 125  
 Phe Val Ile Ser Gly Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe  
 130 135 140

Asp  
 145

&lt;210&gt; 311

&lt;211&gt; 879

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(856)

&lt;223&gt; RXN02515

&lt;400&gt; 311

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tcagtttaaa attcgcttca accctgaaag attgtgacag atg agc act ctt gaa 115
                                         Met Ser Thr Leu Glu
                                         1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
                        10 15 20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
                        25 30 35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
                        40 45 50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
                        55 60 65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
                        70 75 80 85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
                        90 95 100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
                        105 110 115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
                        120 125 130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
                        135 140 145

ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
                        150 155 160 165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
                        170 175 180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
                        185 190 195

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Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr  
195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val  
 210 215 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp  
 225 230 235 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys  
 245 250

<210> 313

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> FRXA02515

<400> 313

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 Met Ser Thr Leu Glu  
 1 5  
 atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163  
 Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu  
 10 15 20  
 cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211  
 Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu  
 25 30 35  
 atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259  
 Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala  
 40 45 50  
 tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307  
 Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val  
 55 60 65  
 ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355  
 Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala  
 70 75 80 85  
 cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403  
 Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly  
 90 95 100  
 gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451  
 Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly  
 105 110 115  
 gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499  
 Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln  
 120 125 130  
 gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547

Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu  
 135 140 145  
 ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595  
 Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp  
 150 155 160 165  
 ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643  
 Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu  
 170 175 180  
 gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691  
 Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys  
 185 190 195  
 cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739  
 Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile  
 200 205 210  
 ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787  
 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln  
 215 220 225  
 att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac 835  
 Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp  
 230 235 240 245  
 ggc tac gac cag ttc atc aag taacatgtcc gatttctca atg 879  
 Gly Tyr Asp Gln Phe Ile Lys  
 250

&lt;210&gt; 314

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 314

Met Ser Thr Leu Glu Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser  
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 Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr  
 20 25 30  
 Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly  
 35 40 45  
 Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val  
 50 55 60  
 Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu  
 65 70 75 80  
 Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro  
 85 90 95  
 Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala  
 100 105 110  
 Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu  
 115 120 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn  
 130 135 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu  
 145 150 155 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu  
 165 170 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly  
 180 185 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr  
 195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val  
 210 215 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp  
 225 230 235 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys  
 245 250

<210> 315  
 <211> 1461  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1438)  
 <223> RXN01995

<400> 315  
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 Met Asp Ile Arg Gln  
 1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163  
 Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe  
 10 15 20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211  
 Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met  
 25 30 35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259  
 Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser  
 40 45 50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307  
 Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly  
 55 60 65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355  
 Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala

70	75	80	85	
ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc				403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala	90	95	100	
acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt				451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly	105	110	115	
atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag				499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu	120	125	130	
ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct				547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala	135	140	145	
ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc				595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu	150	155	160	165
atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca				643
Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala	170	175	180	
act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt				691
Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val	185	190	195	
gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat				739
Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn	200	205	210	
tac att gcg cgc cgc ctg ggc aaa gtc ggt acc ttt gag ctt cca ggc				787
Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr Phe Glu Leu Pro Gly	215	220	225	
gaa caa agc ttg tcg acg aaa aaa gcc ggt ctc caa tcg tat gca gtg				835
Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu Gln Ser Tyr Ala Val	230	235	240	245
ctc gtt aac aaa gag aac cgt gga acc agc atc aag ctg tgg gtt gcg				883
Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile Lys Leu Trp Val Ala	250	255	260	
ttc ggc atc gtg atg ttc ggc ttc tac ttc gcc aac act tgg acc ccg				931
Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala Asn Thr Trp Thr Pro	265	270	275	
aag ctg ctc gtg gaa acc gga atg tca gaa cag cag ggc atc atc ggt				979
Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln Gln Gly Ile Ile Gly	280	285	290	
ggt ttg atg ttg tcc atg ggt gga gca ttc ggc tcc ctg ctc tac ggt				1027
Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly Ser Leu Leu Tyr Gly	295	300	305	
ttc ctc acc acc aag ttc agc tcc cga aac aca ctg atg acc ttc atg				1075
Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr Leu Met Thr Phe Met	310	315	320	325

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 Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile Ser Ser Thr Ser Val  
                   330                                  335                                  340

cca tcc atc gcg ttt gcc agc ggc gtt gtc gtg ggc atg ctg atc aat 1171  
 Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val Gly Met Leu Ile Asn  
                   345                                  350                                  355

ggt tgt gtg gct ggt ctg tac acc ctg tcc cca cag ctg tac tcc gct 1219  
 Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro Gln Leu Tyr Ser Ala  
                   360                                  365                                  370

gaa gta cgc acc act ggt gtg ggc gct gcg att ggt atg ggt cgt gtc 1267  
 Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile Gly Met Gly Arg Val  
                   375                                  380                                  385

ggt gcg att tcc gcg cca ctg ctg gtg ggt ggc ctg ctg gat tct ggc 1315  
 Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly Leu Leu Asp Ser Gly  
                   390                                  395                                  400                                  405

tgg tcc cca acg cag ctg tat gtt ggt gtg gca gtg att gtt att gcc 1363  
 Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala Val Ile Val Ile Ala  
                   410                                  415                                  420

ggt gca acc gca ttg att ggg atg cgc act cag gcg gta gcc gtc gaa 1411  
 Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln Ala Val Ala Val Glu  
                   425                                  430                                  435

aag cag cct gaa gcc cta gcg acc aaa tagggccgcg attcctagca tgc 1461  
 Lys Gln Pro Glu Ala Leu Ala Thr Lys  
                   440                                  445

&lt;210&gt; 316

&lt;211&gt; 446

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 316

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                   20                                  25                                  30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe  
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Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe  
                   50                                  55                                  60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe  
                   65                                  70                                  75                                  80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly  
                   85                                  90                                  95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp  
                   100                                  105                                  110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr  
 115 120 125  
 Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met  
 130 135 140  
 Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe  
 145 150 155 160  
 Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala  
 165 170 175  
 Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe  
 180 185 190  
 Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala  
 195 200 205  
 Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr  
 210 215 220  
 Phe Glu Leu Pro Gly Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu  
 225 230 235 240  
 Gln Ser Tyr Ala Val Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile  
 245 250 255  
 Lys Leu Trp Val Ala Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala  
 260 265 270  
 Asn Thr Trp Thr Pro Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln  
 275 280 285  
 Gln Gly Ile Ile Gly Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly  
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 Ser Leu Leu Tyr Gly Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr  
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 Ser Ser Thr Ser Val Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val  
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 Gly Met Leu Ile Asn Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro  
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 Gln Leu Tyr Ser Ala Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile  
 370 375 380  
 Gly Met Gly Arg Val Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly  
 385 390 395 400  
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445

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<223> FRXA01995
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Met Asp Ile Arg Gln															5
1															
aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt															163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe															20
10 15															
atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg															211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met															35
25 30															
tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc															259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser															50
40 45															
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Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly															65
55 60															
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Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala															85
70 75 80															
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Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala															100
90 95															
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Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly															115
105 110															
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Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu															130
120 125															
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Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala															145
135 140															
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Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu															165
150 155 160															
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Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala  
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act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt 691  
 Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val  
 185 190 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat 739  
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 Tyr Ile Ala Arg Arg  
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Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe  
 35 40 45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe  
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Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe  
 65 70 75 80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly  
 85 90 95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp  
 100 105 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr  
 115 120 125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met  
 130 135 140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe  
 145 150 155 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala  
 165 170 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe  
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 195 200 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg  
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Met Met Asn Gly Val  
1 5  
gta cag cct cag gaa cat ctc gat gca acg ttg att gct gca gac ttc 163  
Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu Ile Ala Ala Asp Phe  
10 15 20  
cac ggc aac ccc gaa aac tct ggt gac cgc aaa gag cgc ctg aat ttt 211  
His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys Glu Arg Leu Asn Phe  
25 30 35  
caa ggt tgg aag tat gcc ctt aat cgc acg gtc agg gat gtt ttt cca 259  
Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val Arg Asp Val Phe Pro  
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Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr Phe Phe Ser Ile Leu  
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Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser Val Ile Thr Ile Phe  
70 75 80 85  
ctg gcc agt gac tcc acc gaa atc ctc aac ctt gtc cgc gat gag gta 403  
Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu Val Arg Asp Glu Val  
90 95 100  
aat cag tac gtt ccg gaa gat caa tcc cat gtt gtc aac ggc gtg att 451  
Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val Val Asn Gly Val Ile  
105 110 115  
gat tcg atc gca ggc tcg gca gct gca ggt cag gtc ggt gtc gcg gtc 499  
Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln Val Gly Val Ala Val  
120 125 130  
ggt gtg atc acg gca ttg tgg aca tct tcg gca tat gtg cgc gct ttt 547  
Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala Tyr Val Arg Ala Phe  
135 140 145  
tcc aga tgt gcc aac gct gtt tat ggc cga agc gaa ggc cgc aca ttg 595  
Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser Glu Gly Arg Thr Leu  
150 155 160 165

atc aaa cgc tgg gca atg ctg ctt ttc ctc aac ctt gct ttg ctg ctt 643  
 Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn Leu Ala Leu Leu Leu  
 170 175 180

gga atc atc atc att ttg gtc tcc tgg gtg ctc aac gag acc ttg gtg 691  
 Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu Asn Glu Thr Leu Val  
 185 190 195

atg gga att ttc gcc ccc atc gcg gaa cca ctt cat ctc acg aat gtg 739  
 Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu His Leu Thr Asn Val  
 200 205 210

ctc agc ttc ctc acg gac cgg ttc atg ccg atc tgg atc tgg gtg cgg 787  
 Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile Trp Ile Trp Val Arg  
 215 220 225

ttc cca gtg att gtg ggg gtg ctc atc atg ttc gtg gcc acg ctg tat 835  
 Phe Pro Val Ile Val Gly Val Leu Ile Met Phe Val Ala Thr Leu Tyr  
 230 235 240 245

tac tgg gcc ccg aac gcc cgc ccg tgg aag ttt cgc tgg ctc agc ctc 883  
 Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe Arg Trp Leu Ser Leu  
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gga tca ttc ttg gcg atc gtt ggc atc ctg ctc gca ggc gtg ggc ttg 931  
 Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu Ala Gly Val Gly Leu  
 265 270 275

aat ttc tac ttc acg ctg ttc gcc gct ttt agt tcc tac ggc gcg gtg 979  
 Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser Ser Tyr Gly Ala Val  
 280 285 290

ggt tcg ctg ctc gcg gtt ttt att gcg ctg tgg gtg ttc aac att tgc 1027  
 Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp Val Phe Asn Ile Cys  
 295 300 305

tta atc atc ggc ctg aaa atc gac gtg gag atc agc cgc gcc aag caa 1075  
 Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile Ser Arg Ala Lys Gln  
 310 315 320 325

ctg cag gca gga atg ccg gcg gag gat tac agt tta gtg cca cca cgc 1123  
 Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser Leu Val Pro Pro Arg  
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tct atc gag aag gtg gcg aaa atg aag cag cgc cag cag cgc ttg atg 1171  
 Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg Gln Gln Arg Leu Met  
 345 350 355

gat cag gct gcg gcg atc cgg gag gaa agc aat taaaaaattg cttatcgacg 1224  
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<213> Corynebacterium glutamicum

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 35 40 45  
 Arg Asp Val Phe Pro Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr  
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 Phe Phe Ser Ile Leu Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser  
 65 70 75 80  
 Val Ile Thr Ile Phe Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu  
 85 90 95  
 Val Arg Asp Glu Val Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val  
 100 105 110  
 Val Asn Gly Val Ile Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln  
 115 120 125  
 Val Gly Val Ala Val Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala  
 130 135 140  
 Tyr Val Arg Ala Phe Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser  
 145 150 155 160  
 Glu Gly Arg Thr Leu Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn  
 165 170 175  
 Leu Ala Leu Leu Leu Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu  
 180 185 190  
 Asn Glu Thr Leu Val Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu  
 195 200 205  
 His Leu Thr Asn Val Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile  
 210 215 220  
 Trp Ile Trp Val Arg Phe Pro Val Ile Val Gly Val Leu Ile Met Phe  
 225 230 235 240  
 Val Ala Thr Leu Tyr Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe  
 245 250 255  
 Arg Trp Leu Ser Leu Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu  
 260 265 270  
 Ala Gly Val Gly Leu Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser  
 275 280 285  
 Ser Tyr Gly Ala Val Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp  
 290 295 300  
 Val Phe Asn Ile Cys Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile  
 305 310 315 320  
 Ser Arg Ala Lys Gln Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser

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Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn Ile Asp Asp Ile Ile																		
	10			15				20										
gtg CTC tcg ctg ttt ttt gcc CGC ggg gcg ggg caa aaa ggg acc acg	211																	
Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly Gln Lys Gly Thr Thr																		
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CTT cgG att ctg gct ggt cag tac CTC ggC ttC atG ggC atC CTC gcg	259																	
Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe Met Gly Ile Leu Ala																		
	40			45				50										
gcc gCa gtC ctG gtC acG ctG gGG gCa gGa gCa ttC CtA cCt gCt gag	307																	
Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala Phe Leu Pro Ala Glu																		
	55			60				65										
gcg atC ccG taC ttC gGa CtA att CCc CTg gcC ctG gGa CtA tgG gcg	355																	
Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala Leu Gly Leu Trp Ala																		
	70			75				80			85							
gcc tgG caG gcc tgG cGa agC gat gat gaC gaC gat gat gat gcg gag	403																	
Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp Asp Asp Ala Glu																		
	90			95				100										
aTC gcC ggG aaA aAG gtG gGT gtG CTg acc gtc gcc ggt gtG acG tTT	451																	
Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val Ala Gly Val Thr Phe																		
	105			110				115										
gcc aAC gGT ggC gaC aAT aTC ggC gtc taC gtc CCg gtc ttC CTC aAc	499																	
Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val Pro Val Phe Leu Asn																		
	120			125				130										
gtG gaC act gcc gcc gtc atC atC taC tgC atC gtt ttC CTC gtc ctG	547																	
Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile Val Phe Leu Val Leu																		
	135			140				145										

gtg gca ggc ctg gtc ctg ctg gca aag ttc gtg gcc acc cgc ccg ccc 595  
 Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val Ala Thr Arg Pro Pro  
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atc gca gaa gtc ctt gag cgc tgg gag cac gtg ctg ttc ccg atc gtc 643  
 Ile Ala Glu Val Leu Glu Arg Trp Glu His Val Leu Phe Pro Ile Val  
 170 175 180

ctg atc ggc ctg ggc atc ttc atc ctc gtc agc ggc ggc gcc ttc ggc 691  
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<210> 322

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

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Ile Asp Asp Ile Ile Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly  
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Gln Lys Gly Thr Thr Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe  
 35 40 45

Met Gly Ile Leu Ala Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala  
 50 55 60

Phe Leu Pro Ala Glu Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala  
 65 70 75 80

Leu Gly Leu Trp Ala Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp  
 85 90 95

Asp Asp Asp Ala Glu Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val  
 100 105 110

Ala Gly Val Thr Phe Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val  
 115 120 125

Pro Val Phe Leu Asn Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile  
 130 135 140

Val Phe Leu Val Leu Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val  
 145 150 155 160

Ala Thr Arg Pro Pro Ile Ala Glu Val Leu Glu Arg Trp Glu His Val  
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Met Glu His Ser Pro																	
1 5																	
gaa ggc aag cgt gga ttc ttc acc tca tgc gtg atg gcg ggt tgc tca																	163
Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val Met Ala Gly Cys Ser																	
10 15 20																	
gtt gga aac gtc ctg gct ggc ttg gta ttt atc ccg ttc ttg atg ctg																	211
Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile Pro Phe Leu Met Leu																	
25 30 35																	
ccg gaa gaa cac ctc atg tca tgg ggc tgg cgc gta cct ttc ctg ctt																	259
Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg Val Pro Phe Leu Leu																	
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Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val Arg Thr Arg Leu Glu																	
55 60 65																	
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Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala Gly Ala Pro Ala Leu																	
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Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala Arg Val Phe Leu Ile																	
90 95 100																	
acc ttc ttc gcc gtt gtt cag acc act ttc aac gtt tac gca ctg gca																	451
Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn Val Tyr Ala Leu Ala																	
105 110 115																	
tac gcc gcc aac gaa atc ggc atc gat cgt tcc ttc atg gtg atg gtg																	499
Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser Phe Met Val Met Val																	
120 125 130																	
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Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr Ile Pro Leu Ala Ala																	
135 140 145																	
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Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val Leu Leu Phe Gly Ala																	
150 155 160 165																	
atc acc tgt gca atc acc acc tac ttc tac ttc cag gca atc tct gaa																	643



Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe Gln Ala Ile Ser Glu  
 170 175 180

gct gac ctt gtg ctg atc ttc gca ctg tgc ttg gtc aac caa ggt ttg 691  
 Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu Val Asn Gln Gly Leu  
 185 190 195

ttc tac tcc tgc tgg aac ggc gtg tgg acc att ttc ttc cca gaa atg 739  
 Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile Phe Phe Pro Glu Met  
 200 205 210

ttc gca tct tcc gtg cgc tac acc ggc atg gct atg ggc aac cag ctc 787  
 Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala Met Gly Asn Gln Leu  
 215 220 225

ggt ctg atc atc gtt ggt ttc gca cca acc atc gcc acc gcc ctg tac 835  
 Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr  
 230 235 240 245

gca tgg aac ggt tgg gaa gct gtt gcg gga ttc atc atc ggc gca atc 883  
 Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe Ile Ile Gly Ala Ile  
 250 255 260

gca ctg tct gcc gca gtt att ttg acc acc aag gaa acc gcc ttc acc 931  
 Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys Glu Thr Ala Phe Thr  
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aag ctt gaa gat cta ggg aag aaa taatgtctga caagatctgg aaa 978  
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 280 285

&lt;210&gt; 324

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 324

Met Glu His Ser Pro Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val  
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Pro Phe Leu Met Leu Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg  
 35 40 45

Val Pro Phe Leu Leu Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val  
 50 55 60

Arg Thr Arg Leu Glu Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala  
 65 70 75 80

Gly Ala Pro Ala Leu Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala  
 85 90 95

Arg Val Phe Leu Ile Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn  
 100 105 110

Val Tyr Ala Leu Ala Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser  
 115 120 125

Phe Met Val Met Val Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr  
 130 135 140  
 Ile Pro Leu Ala Ala Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val  
 145 150 155 160  
 Leu Leu Phe Gly Ala Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe  
 165 170 175  
 Gln Ala Ile Ser Glu Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu  
 180 185 190  
 Val Asn Gln Gly Leu Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile  
 195 200 205  
 Phe Phe Pro Glu Met Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala  
 210 215 220  
 Met Gly Asn Gln Leu Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile  
 225 230 235 240  
 Ala Thr Ala Leu Tyr Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe  
 245 250 255  
 Ile Ile Gly Ala Ile Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys  
 260 265 270  
 Glu Thr Ala Phe Thr Lys Leu Glu Asp Leu Gly Lys Lys  
 275 280 285

&lt;210&gt; 325

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(526)

&lt;223&gt; RXA00312

&lt;400&gt; 325

ccattgaatg ggaagaactt ggttgtgtgt ttgtgacacc tattctaaag aacattaaac 60

gtgattaagt tcatgattct taatgagaaa gggatgatcac atg gaa acc gtg agg 115  
 Met Glu Thr Val Arg  
 1 5

acc gca acc gcc gct cct gaa act gca tct ttg aag ctg cgt gag gca 163  
 Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu Lys Leu Arg Glu Ala  
 10 15 20

gaa agc cca gca aag tcc cca aag aaa gcc gcc ttg gcg tca ctt ttg 211  
 Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala Leu Ala Ser Leu Leu  
 25 30 35

ggt tcg act ctg gag tac tac gac ttt gtc att tac ggc acc gcc tcc 259  
 Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile Tyr Gly Thr Ala Ser  
 40 45 50

gcg ctg ctg ttc aat cac ctc ttc ttc cca cag ggc gac cca gtc gtc 307  
 Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln Gly Asp Pro Val Val  
     55                    60                    65

gcg acg atc ggc tct ctc gcc tca ttc ggt gtt gcg tac att gcg cgc 355  
 Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val Ala Tyr Ile Ala Arg  
     70                    75                    80                    85

ccc atc ggt ggt ctg gtg atg gga cat gtt ggc gat aag atc agt cgc 403  
 Pro Ile Gly Gly Leu Val Met Gly His Val Gly Asp Lys Ile Ser Arg  
                     90                    95                    100

aaa acc gcc ctc atg gtg acg ttg atg atc atg ggt atc gcc tcc att 451  
 Lys Thr Ala Leu Met Val Thr Leu Met Ile Met Gly Ile Ala Ser Ile  
                     105                    110                    115

tcc atc gga ctt ctg ccc acc tac gga cag atc ggc att tgg gcg acc 499  
 Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile Gly Ile Trp Ala Thr  
     120                    125                    130

gtg ctg ttg atg atc gcc cgc atc gca tagggattct ctgcagtcgc aga 549  
 Val Leu Leu Met Ile Ala Arg Ile Ala  
     135                    140

<210> 326

<211> 142

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 326

Met Glu Thr Val Arg Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu  
     1                    5                    10                    15

Lys Leu Arg Glu Ala Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala  
             20                    25                    30

Leu Ala Ser Leu Leu Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile  
             35                    40                    45

Tyr Gly Thr Ala Ser Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln  
     50                    55                    60

Gly Asp Pro Val Val Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val  
     65                    70                    75                    80

Ala Tyr Ile Ala Arg Pro Ile Gly Gly Leu Val Met Gly His Val Gly  
             85                    90                    95

Asp Lys Ile Ser Arg Lys Thr Ala Leu Met Val Thr Leu Met Ile Met  
             100                    105                    110

Gly Ile Ala Ser Ile Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile  
     115                    120                    125

Gly Ile Trp Ala Thr Val Leu Leu Met Ile Ala Arg Ile Ala  
     130                    135                    140

<210> 327

<211> 888

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(865)

&lt;223&gt; RXN01411

&lt;400&gt; 327

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cttatcgacg tccccatccc cctcgccaat gcttcggcga ggggttctat ttattgtgtg 60

tgctagcctt ttcgcaatcg ttcagcccgc cccgacgtca atg ttg gga gtg ggc 115
                                         Met Leu Gly Val Gly
                                         1                               5

tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg 163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp
                        10                               15                               20

tgg atc cgc acc ggt gcc cag gaa aat gta cgc ccc gca tcc gaa cgc 211
Trp Ile Arg Thr Gly Ala Gln Glu Asn Val Arg Pro Ala Ser Glu Arg
                        25                               30                               35

ccc gaa gct cct att aag cag gca ttg cgt act gag tgg aag atg atg 259
Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met
                        40                               45                               50

ttg cgg gta ggt ggc ttt atc tct tgc acc ggt ctg agc ttc tac att 307
Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly Leu Ser Phe Tyr Ile
                        55                               60                               65

ttc acc acg tac atg acc act ttc ctg cgc agc acc gtc gga ctg gag 355
Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser Thr Val Gly Leu Glu
                        70                               75                               80                               85

ggc acg tta gtg ctg gct gga aac atc atc gct ctc agc atg gca gca 403
Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala Leu Ser Met Ala Ala
                        90                               95                               100

att gtg gcc cca ttt gtt ggc cgc gca att gat aaa ttc ccc cgc cgg 451
Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp Lys Phe Pro Arg Arg
                        105                               110                               115

aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg 499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro
                        120                               125                               130

gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg 547
Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr Ala Ser Leu Ile Ala
                        135                               140                               145

cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca 595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser
                        150                               155                               160                               165

gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt act tcc gcc 643
Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly Thr Ser Ala
                        170                               175                               180

ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca 691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro

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185										190					195					
ttt	atc	tcc	acc	gca	ttg	gtc	tcc	tgg	acc	ggc	agc	ccg	ctg	gcc	cct	739				
Phe	Ile	Ser	Thr	Ala	Leu	Val	Ser	Trp	Thr	Gly	Ser	Pro	Leu	Ala	Pro					
		200					205					210								
gcg	gta	tac	atg	atc	atc	att	gcg	ctc	ttc	gcc	ttc	acc	gcg	tcc	cgc	787				
Ala	Val	Tyr	Met	Ile	Ile	Ile	Ala	Leu	Phe	Ala	Phe	Thr	Ala	Ser	Arg					
	215					220					225									
ttc	att	cct	gaa	acc	tcc	cca	gtt	ttt	gtc	acc	gca	acc	ccg	gcc	att	835				
Phe	Ile	Pro	Glu	Thr	Ser	Pro	Val	Phe	Val	Thr	Ala	Thr	Pro	Ala	Ile					
230					235				240					245						
aag	gca	cca	aag	gtg	ctg	gtc	aac	ccg	ggc	taa	acc	acgc	ttttc	gcacga		885				
Lys	Ala	Pro	Lys	Val	Leu	Val	Asn	Pro	Gly											
			250					255												
aaa																888				

&lt;210&gt; 328

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 328

Met	Leu	Gly	Val	Gly	Trp	Arg	Ile	Pro	Phe	Leu	Met	Ala	Val	Pro	Leu
1				5					10					15	
Gly	Leu	Ile	Gly	Trp	Trp	Ile	Arg	Thr	Gly	Ala	Gln	Glu	Asn	Val	Arg
			20					25					30		
Pro	Ala	Ser	Glu	Arg	Pro	Glu	Ala	Pro	Ile	Lys	Gln	Ala	Leu	Arg	Thr
		35					40					45			
Glu	Trp	Lys	Met	Met	Leu	Arg	Val	Gly	Gly	Phe	Ile	Ser	Cys	Thr	Gly
	50					55					60				
Leu	Ser	Phe	Tyr	Ile	Phe	Thr	Thr	Tyr	Met	Thr	Thr	Phe	Leu	Arg	Ser
	65				70					75					80
Thr	Val	Gly	Leu	Glu	Gly	Thr	Leu	Val	Leu	Ala	Gly	Asn	Ile	Ile	Ala
				85					90					95	
Leu	Ser	Met	Ala	Ala	Ile	Val	Ala	Pro	Phe	Val	Gly	Arg	Ala	Ile	Asp
			100					105					110		
Lys	Phe	Pro	Arg	Arg	Asn	Ile	Met	Ala	Phe	Ala	Thr	Leu	Ser	Thr	Val
		115					120					125			
Ile	Met	Ala	Ile	Pro	Ala	Tyr	Ile	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Thr
	130					135					140				
Ala	Ser	Leu	Ile	Ala	Gln	Val	Met	Leu	Gly	Ile	Gly	Ala	Val	Thr	Ala
145					150					155					160
Asn	Cys	Val	Thr	Ser	Val	Met	Met	Ala	Glu	Val	Phe	Gln	Glu	Val	Thr
				165					170					175	
Arg	Gly	Thr	Ser	Ala	Gly	Ile	Thr	Tyr	Asn	Val	Thr	Tyr	Ala	Ile	Phe

180	185	190
Gly Gly Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly		
195	200	205
Ser Pro Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala		
210	215	220
Phe Thr Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr		
225	230	235
Ala Thr Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly		
245	250	255

&lt;210&gt; 329

&lt;211&gt; 350

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(327)

&lt;223&gt; FRXA01411

&lt;400&gt; 329

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Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys	
1 5 10 15	
gtt acc tca gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt	96
Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly	
20 25 30	
act tcc gcc ggc att acc tac aac gtc act tac gca atc ttc ggc ggc	144
Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly	
35 40 45	
tcg gct cca ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg	192
Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro	
50 55 60	
ctg gcc cct gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc	240
Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr	
65 70 75 80	
gcg tcc cgc ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc	288
Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr	
85 90 95	
ccg gcc att aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc	337
Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly	
100 105	
ttttcgacga aaa	350

&lt;210&gt; 330

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys  
 1 5 10 15  
 Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly  
 20 25 30  
 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly  
 35 40 45  
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro  
 50 55 60  
 Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr  
 65 70 75 80  
 Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr  
 85 90 95  
 Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly  
 100 105

&lt;210&gt; 331

&lt;211&gt; 1422

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1399)

&lt;223&gt; RXA01900

&lt;400&gt; 331

aaaggtgaca cgccttacat tcttgtggtc tgaccatgag gttggggccaa tcggttttcag 60  
 cccgttttact cccgcggtcc gtttcagaga agaggtcacc atg aca acc gca gta 115  
 Met Thr Thr Ala Val  
 1 5  
 gat caa aac tca ccg ccc aag cag caa ctc aac aag cgc gtc ctg ctg 163  
 Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn Lys Arg Val Leu Leu  
 10 15 20  
 ggc agc ttg agt ggc agc gtt atc gaa tgg ttc gac ttc ctg gtt tac 211  
 Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe Asp Phe Leu Val Tyr  
 25 30 35  
 gga acc gtc gcc gcg ctg gtc ttc aac aag atg tac ttc ccc agc ggc 259  
 Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met Tyr Phe Pro Ser Gly  
 40 45 50  
 aac gag ttc ctc tcc aca atc ctg gcg tac gca tcc ttc tcc ctg acc 307  
 Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala Ser Phe Ser Leu Thr  
 55 60 65  
 ttc ttc ttc cgc ccc att ggt ggc gtc atc ttc gcc cac atc ggc gac 355  
 Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe Ala His Ile Gly Asp  
 70 75 80 85

cgc att ggg cgt aag aag acc ctg ttc atc acc ttg atg ctc atg ggt Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr Leu Met Leu Met Gly	403
90 95 100	
ggc ggc acc gtc gcc att ggt ttg ctg ccc gac tac aac gcc atc ggc Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp Tyr Asn Ala Ile Gly	451
105 110 115	
att tgg gca cca atc ctt ctg atg ttc ctc cgc att ttg cag ggc atc Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg Ile Leu Gln Gly Ile	499
120 125 130	
gga att ggc ggc gaa tgg ggt ggc gca ctg ctc ctg gca tac gaa tac Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu Leu Ala Tyr Glu Tyr	547
135 140 145	
gct cca aag aag cag cgt ggg ctc tac ggc gca gtt cct caa atg ggc Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala Val Pro Gln Met Gly	595
150 155 160 165	
att tcc ctg ggc atg ctg ctt gca gct ggc gtg atc tct ctg ctc acc Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val Ile Ser Leu Leu Thr	643
170 175 180	
ctc atg ccg gaa gat cag ttc ctc acc tgg ggc tgg cgc atc cca ttc Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly Trp Arg Ile Pro Phe	691
185 190 195	
gtc gga tcc atc ctc cta gtg ttc atc ggc ctg ttc atc cga aac ggc Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu Phe Ile Arg Asn Gly	739
200 205 210	
ctt gat gaa acc ccc gag ttc aag cgt atc cgc gat tcc ggc cag cag Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg Asp Ser Gly Gln Gln	787
215 220 225	
gta aag atg cct ctg aag gaa gtt ctg acc aag tac tgg cca gcc gtt Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys Tyr Trp Pro Ala Val	835
230 235 240 245	
ctg gtc tcc atc ggc gca aaa gct gcc gag acc ggc ccc ttc tac atc Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr Gly Pro Phe Tyr Ile	883
250 255 260	
ttc ggc acc tac atc gtt gct tac gca acc aac ttc ctg aac atc cgc Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn Phe Leu Asn Ile Arg	931
265 270 275	
gac aac att gtc ctt ctg gca gtt gct tgc gcc gcc ctc gtt gcc acc Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala Ala Leu Val Ala Thr	979
280 285 290	
atc tgg atg cca ctg ttc gga tcc ttc tcc gac cgc gtc aac cgt gca Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp Arg Val Asn Arg Ala	1027
295 300 305	
gtg ctc tac agg atc tgt gca tcc gca acc atc gtg ctg att gtc cct Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile Val Leu Ile Val Pro	1075
310 315 320 325	
tac tac ttg gtc ctc aac acc ggc gaa att tgg gca ctg ttt atc act	1123



Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp Ala Leu Phe Ile Thr  
 330 335 340  
 acc gtg att ggc ttc ggc atc ctc tgg ggt agc gtc aac gca atc ctc 1171  
 Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser Val Asn Ala Ile Leu  
 345 350 355  
 gga acc gtc atc gca gaa aac ttc gca cct gag gtc cgc tac acc ggc 1219  
 Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu Val Arg Tyr Thr Gly  
 360 365 370  
 gct acc ctg ggt tac caa gtc gga gca gca ctc ttc ggc ggt acc gca 1267  
 Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu Phe Gly Gly Thr Ala  
 375 380 385  
 ccc att atc gca gca tgg ctg ttc gaa atc tcc ggc gga caa tgg tgg 1315  
 Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser Gly Gly Gln Trp Trp  
 390 395 400 405  
 cca atc gcc gtc tac gtc gct gca tgt tgc ctt ctc tct gtg atc gcc 1363  
 Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu Leu Ser Val Ile Ala  
 410 415 420  
 tcg ttc ttc atc caa cgc gtc gcg cac caa gag aac taaaatctaa 1409  
 Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu Asn  
 425 430  
 gtaaaacccc tcc 1422  
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 <211> 433  
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 <213> Corynebacterium glutamicum  
 <400> 332  
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 Asp Phe Leu Val Tyr Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met  
 35 40 45  
 Tyr Phe Pro Ser Gly Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala  
 50 55 60  
 Ser Phe Ser Leu Thr Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe  
 65 70 75 80  
 Ala His Ile Gly Asp Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr  
 85 90 95  
 Leu Met Leu Met Gly Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp  
 100 105 110  
 Tyr Asn Ala Ile Gly Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg  
 115 120 125  
 Ile Leu Gln Gly Ile Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu

130	135	140
Leu Ala Tyr Glu Tyr	Ala Pro Lys Lys Gln Arg	Gly Leu Tyr Gly Ala
145	150	155 160
Val Pro Gln Met	Gly Ile Ser Leu Gly Met	Leu Leu Ala Ala Gly Val
	165	170 175
Ile Ser Leu Leu Thr	Leu Met Pro Glu Asp Gln Phe	Leu Thr Trp Gly
	180	185 190
Trp Arg Ile Pro Phe Val	Gly Ser Ile Leu Leu Val	Phe Ile Gly Leu
	195	200 205
Phe Ile Arg Asn Gly	Leu Asp Glu Thr Pro Glu	Phe Lys Arg Ile Arg
	210	215 220
Asp Ser Gly Gln Gln	Val Lys Met Pro Leu Lys Glu	Val Leu Thr Lys
	225	230 235 240
Tyr Trp Pro Ala Val	Leu Val Ser Ile Gly Ala Lys	Ala Ala Glu Thr
	245	250 255
Gly Pro Phe Tyr Ile	Phe Gly Thr Tyr Ile Val	Ala Tyr Ala Thr Asn
	260	265 270
Phe Leu Asn Ile Arg	Asp Asn Ile Val Leu Leu	Ala Val Ala Cys Ala
	275	280 285
Ala Leu Val Ala Thr	Ile Trp Met Pro Leu Phe	Gly Ser Phe Ser Asp
	290	295 300
Arg Val Asn Arg Ala	Val Leu Tyr Arg Ile Cys	Ala Ser Ala Thr Ile
	305	310 315 320
Val Leu Ile Val Pro	Tyr Tyr Leu Val Leu Asn	Thr Gly Glu Ile Trp
	325	330 335
Ala Leu Phe Ile Thr	Thr Val Ile Gly Phe Gly	Ile Leu Trp Gly Ser
	340	345 350
Val Asn Ala Ile Leu	Gly Thr Val Ile Ala Glu	Asn Phe Ala Pro Glu
	355	360 365
Val Arg Tyr Thr Gly	Ala Thr Leu Gly Tyr Gln	Val Gly Ala Ala Leu
	370	375 380
Phe Gly Gly Thr Ala	Pro Ile Ile Ala Ala Trp	Leu Phe Glu Ile Ser
	385	390 395 400
Gly Gly Gln Trp Trp	Pro Ile Ala Val Tyr Val	Ala Ala Cys Cys Leu
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Leu Ser Val Ile Ala	Ser Phe Phe Ile Gln Arg	Val Ala His Gln Glu
	420	425 430

Asn

&lt;210&gt; 333

<211> 1524  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1501)  
 <223> RXA02507

<400> 333

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                                         Met Ser Glu Gln Leu
                                         1                               5

cag ggt gta act cac tcc gaa tca act ccg ggc aag acg ccc aag cga 163
Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly Lys Thr Pro Lys Arg
                        10                        15                        20

gca gca cta tcc agc tgg atc ggc tca gct ctc gaa tac tac gac ttc 211
Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu Glu Tyr Tyr Asp Phe
                        25                        30                        35

gct gtt tac gga acc gct gca gcg ctg gtt ctt aac cac ctc ttc ttc 259
Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu Asn His Leu Phe Phe
                        40                        45                        50

cca gct gat act tca cca ggc atc gca att ttg gct gcg atg ggt acc 307
Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu Ala Ala Met Gly Thr
                        55                        60                        65

gtg ggt gtt gct tat gtg gtt cgc cct ctt ggt gcg ctg atc atg ggt 355
Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly Ala Leu Ile Met Gly
70                        75                        80                        85

cca tta ggt gac cgt tac gga cgt aaa ttt gtc ctc atg ctg tgc ctc 403
Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val Leu Met Leu Cys Leu
                        90                        95                        100

ttc ctg att gga gca tcc act ttc gca gtt ggc tgc ttg cca aca ttt 451
Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly Cys Leu Pro Thr Phe
                        105                        110                        115

gat cag gtc ggt tac ttg gct ccg gca ctg ttg gtg ctg tgc cgt gtg 499
Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu Val Leu Cys Arg Val
                        120                        125                        130

atc cag gga ctg tct gca tcc ggt gag cag tcc agt gcg att tcc gtt 547
Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser Ser Ala Ile Ser Val
                        135                        140                        145

tct ttg gag cac gcc gat gag cgt cac cgc gca ttt act gct agc tgg 595
Ser Leu Glu His Ala Asp Glu Arg His Arg Ala Phe Thr Ala Ser Trp
150                        155                        160                        165

act ctt cac gga acc cag ttc ggt acc ttg ctg gca acc gga gta ttt 643
Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu Ala Thr Gly Val Phe
                        170                        175                        180

atc cca ttc acc ttg ttc ctg agt gaa gat gct cta atg tca tgg ggt 691

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Ile	Pro	Phe	Thr	Leu	Phe	Leu	Ser	Glu	Asp	Ala	Leu	Met	Ser	Trp	Gly		
			185					190					195				
tgg	cgc	gtt	ccg	ttc	tgg	ctg	tcc	gct	gct	gtt	gtt	ttg	gtt	gct	ttc	739	
Trp	Arg	Val	Pro	Phe	Trp	Leu	Ser	Ala	Ala	Val	Val	Leu	Val	Ala	Phe		
		200					205					210					
ctc	atc	cgt	cgt	gga	ctg	gaa	gag	cca	cca	gca	ttc	cgt	gaa	aac	aag	787	
Leu	Ile	Arg	Arg	Gly	Leu	Glu	Glu	Pro	Pro	Ala	Phe	Arg	Glu	Asn	Lys		
	215					220					225						
gaa	gca	gtt	gca	ggc	gca	gca	tct	cca	ctg	gcg	atg	acc	ttg	cgt	tac	835	
Glu	Ala	Val	Ala	Gly	Ala	Ala	Ser	Pro	Leu	Ala	Met	Thr	Leu	Arg	Tyr		
230					235					240					245		
cac	aag	gcg	gcg	gtt	gct	cgc	gtt	gct	att	gct	gcg	atg	atc	aac	tcc	883	
His	Lys	Ala	Ala	Val	Ala	Arg	Val	Ala	Ile	Ala	Ala	Met	Ile	Asn	Ser		
				250					255					260			
gtg	aac	att	gtg	ttt	act	gtg	tgg	gca	ctg	tcg	ttc	gcc	acc	aac	att	931	
Val	Asn	Ile	Val	Phe	Thr	Val	Trp	Ala	Leu	Ser	Phe	Ala	Thr	Asn	Ile		
			265					270					275				
gtt	ggc	ctg	gat	cgt	tca	act	gtt	ttg	ctg	gtt	cca	gtt	gtt	gcg	aac	979	
Val	Gly	Leu	Asp	Arg	Ser	Thr	Val	Leu	Leu	Val	Pro	Val	Val	Ala	Asn		
		280					285					290					
ttg	gtt	gca	ctg	att	gcg	att	cct	ttg	tcc	ggc	atg	ctg	gct	gac	cgc	1027	
Leu	Val	Ala	Leu	Ile	Ala	Ile	Pro	Leu	Ser	Gly	Met	Leu	Ala	Asp	Arg		
	295					300					305						
att	ggc	cgc	cga	cca	gtg	ttc	atc	atg	ggc	gcc	att	ggc	ggc	ggc	ctg	1075	
Ile	Gly	Arg	Arg	Pro	Val	Phe	Ile	Met	Gly	Ala	Ile	Gly	Gly	Gly	Leu		
310					315					320					325		
gcc	atg	aac	ggc	tac	ctg	gga	gct	atc	tac	tcc	ggc	aat	tgg	acc	atg	1123	
Ala	Met	Asn	Gly	Tyr	Leu	Gly	Ala	Ile	Tyr	Ser	Gly	Asn	Trp	Thr	Met		
				330					335					340			
atc	ttc	ttc	atg	ggc	gtg	ttg	atg	tct	ggc	ctg	ctg	tac	tcc	atg	ggc	1171	
Ile	Phe	Phe	Met	Gly	Val	Leu	Met	Ser	Gly	Leu	Leu	Tyr	Ser	Met	Gly		
			345					350					355				
aat	gcc	gtg	tgg	cca	gcg	ttc	tac	gca	gaa	atg	ttc	cca	acc	tct	gtg	1219	
Asn	Ala	Val	Trp	Pro	Ala	Phe	Tyr	Ala	Glu	Met	Phe	Pro	Thr	Ser	Val		
		360					365					370					
cgt	gtc	acc	ggc	ttg	gct	ctt	gga	act	cag	att	ggc	ttc	gca	gtc	tct	1267	
Arg	Val	Thr	Gly	Leu	Ala	Leu	Gly	Thr	Gln	Ile	Gly	Phe	Ala	Val	Ser		
	375					380					385						
ggc	ggc	ttc	gtc	cca	gtt	atc	gca	tcc	gcg	ctt	gct	ggc	gat	cag	ggc	1315	
Gly	Gly	Phe	Val	Pro	Val	Ile	Ala	Ser	Ala	Leu	Ala	Gly	Asp	Gln	Gly		
390					395					400					405		
gac	cag	tgg	atg	aag	gtg	tcc	atc	ttc	gtt	ggc	gtt	gtt	tgt	gtg	att	1363	
Asp	Gln	Trp	Met	Lys	Val	Ser	Ile	Phe	Val	Gly	Val	Val	Cys	Val	Ile		
				410					415					420			
tct	gca	ctg	gtt	gcc	atg	acc	gct	aag	gaa	acc	aag	gct	ctg	act	ctg	1411	
Ser	Ala	Leu	Val	Ala	Met	Thr	Ala	Lys	Glu	Thr	Lys	Ala	Leu	Thr	Leu		

425                      430                      435  
 gat gag atc gat gct ctg cac act gct ggt ggt gag gcc gca gac ctg 1459  
 Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly Glu Ala Ala Asp Leu  
           440                      445                      450  
  
 gca gcc gca agc aaa gcc tcc gag gcc caa ctc gcg gct cag 1501  
 Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu Ala Ala Gln  
           455                      460                      465  
  
 taaaacaaa aggaatcttt gac 1524

&lt;210&gt; 334

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 334

Met Ser Glu Gln Leu Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly  
   1                                  5                                  10                                  15  
  
 Lys Thr Pro Lys Arg Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu  
           20                                  25                                  30  
  
 Glu Tyr Tyr Asp Phe Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu  
           35                                  40                                  45  
  
 Asn His Leu Phe Phe Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu  
           50                                  55                                  60  
  
 Ala Ala Met Gly Thr Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly  
           65                                  70                                  75                                  80  
  
 Ala Leu Ile Met Gly Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val  
                                   85                                  90                                  95  
  
 Leu Met Leu Cys Leu Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly  
                                   100                                  105                                  110  
  
 Cys Leu Pro Thr Phe Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu  
           115                                  120                                  125  
  
 Val Leu Cys Arg Val Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser  
           130                                  135                                  140  
  
 Ser Ala Ile Ser Val Ser Leu Glu His Ala Asp Glu Arg His Arg Ala  
   145                                  150                                  155                                  160  
  
 Phe Thr Ala Ser Trp Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu  
           165                                  170                                  175  
  
 Ala Thr Gly Val Phe Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala  
           180                                  185                                  190  
  
 Leu Met Ser Trp Gly Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val  
           195                                  200                                  205  
  
 Val Leu Val Ala Phe Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala  
           210                                  215                                  220

Phe Arg Glu Asn Lys Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala  
 225 230 235 240  
 Met Thr Leu Arg Tyr His Lys Ala Ala Val Ala Arg Val Ala Ile Ala  
 245 250 255  
 Ala Met Ile Asn Ser Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser  
 260 265 270  
 Phe Ala Thr Asn Ile Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val  
 275 280 285  
 Pro Val Val Ala Asn Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly  
 290 295 300  
 Met Leu Ala Asp Arg Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala  
 305 310 315 320  
 Ile Gly Gly Gly Leu Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser  
 325 330 335  
 Gly Asn Trp Thr Met Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu  
 340 345 350  
 Leu Tyr Ser Met Gly Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met  
 355 360 365  
 Phe Pro Thr Ser Val Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile  
 370 375 380  
 Gly Phe Ala Val Ser Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu  
 385 390 395 400  
 Ala Gly Asp Gln Gly Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly  
 405 410 415  
 Val Val Cys Val Ile Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr  
 420 425 430  
 Lys Ala Leu Thr Leu Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly  
 435 440 445  
 Glu Ala Ala Asp Leu Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu  
 450 455 460  
 Ala Ala Gln  
 465

<210> 335

<211> 955

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (21)..(932)

<223> RXA00445

<400> 335

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Met Ala Asp Leu Ser Ile Glu His Val Ser Arg																
				1					5					10		
ttt	ttc	ggc	gat	gcc	atc	gcc	ttg	aac	gat	gtg	tca	ttg	acc	gtc	ccc	101
Phe	Phe	Gly	Asp	Ala	Ile	Ala	Leu	Asn	Asp	Val	Ser	Leu	Thr	Val	Pro	
				15					20					25		
tca	ggc	tcc	atc	acc	gcc	atc	atc	ggg	ccg	tcc	ggg	agc	ggt	aaa	acc	149
Ser	Gly	Ser	Ile	Thr	Ala	Ile	Ile	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Thr	
				30					35					40		
acg	tta	ctg	cgt	ttg	ctg	gca	ggc	ctt	gat	tca	ccc	gat	gaa	ggc	acc	197
Thr	Leu	Leu	Arg	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Pro	Asp	Glu	Gly	Thr	
				45					50					55		
gtg	agc	att	ggg	aat	aag	atc	gcc	aag	ctg	ggt	gac	act	gcg	ctg	tgt	245
Val	Ser	Ile	Gly	Asn	Lys	Ile	Ala	Lys	Leu	Gly	Asp	Thr	Ala	Leu	Cys	
				60					65					70	75	
ttc	cag	gat	tcg	cct	ttg	tat	ccg	cac	ctt	aat	gtg	tgg	gaa	aac	gtg	293
Phe	Gln	Asp	Ser	Pro	Leu	Tyr	Pro	His	Leu	Asn	Val	Trp	Glu	Asn	Val	
				80					85					90		
gca	ttt	ccg	ctc	aag	ctc	aaa	gcc	acc	aat	act	gca	gat	gag	gtg	gtg	341
Ala	Phe	Pro	Leu	Lys	Leu	Lys	Ala	Thr	Asn	Thr	Ala	Asp	Glu	Val	Val	
				95					100					105		
aaa	aag	cgg	gtg	agt	gat	gtt	ttg	gaa	atg	ctc	gaa	att	gct	ccc	ctc	389
Lys	Lys	Arg	Val	Ser	Asp	Val	Leu	Glu	Met	Leu	Glu	Ile	Ala	Pro	Leu	
				110					115					120		
gcc	cgc	cgg	aaa	att	acc	gaa	ctc	tcc	ggc	ggg	caa	aaa	cag	cgc	gtc	437
Ala	Arg	Arg	Lys	Ile	Thr	Glu	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	
				125					130					135		
ggc	att	gct	cga	gca	ctg	gtc	aga	gac	gta	gag	gtt	tac	ctt	ttc	gac	485
Gly	Ile	Ala	Arg	Ala	Leu	Val	Arg	Asp	Val	Glu	Val	Tyr	Leu	Phe	Asp	
				140					145					150	155	
gaa	ccg	atg	gcc	cac	ctc	gac	caa	gcc	tta	gcc	cgc	gat	att	gtg	gcc	533
Glu	Pro	Met	Ala	His	Leu	Asp	Gln	Ala	Leu	Ala	Arg	Asp	Ile	Val	Ala	
				160					165					170		
gat	ctg	cgc	aaa	att	caa	caa	tcg	ttg	gga	ctg	acg	ttt	gta	tac	gtc	581
Asp	Leu	Arg	Lys	Ile	Gln	Gln	Ser	Leu	Gly	Leu	Thr	Phe	Val	Tyr	Val	
				175					180					185		
acc	cac	agc	aaa	tcc	gag	gca	ttc	gcg	ctc	gcc	gac	caa	att	gtc	gtg	629
Thr	His	Ser	Lys	Ser	Glu	Ala	Phe	Ala	Leu	Ala	Asp	Gln	Ile	Val	Val	
				190					195					200		
ctg	gta	gat	ggc	caa	gtc	gcg	cag	gtt	ggt	gag	gcg	gag	gag	ctc	gtc	677
Leu	Val	Asp	Gly	Gln	Val	Ala	Gln	Val	Gly	Glu	Ala	Glu	Glu	Leu	Val	
				205					210					215		
gaa	aag	cca	aaa	acc	cta	gaa	ata	gcc	gag	ttc	ctc	tcc	ccc	acc	gag	725
Glu	Lys	Pro	Lys	Thr	Leu	Glu	Ile	Ala	Glu	Phe	Leu	Ser	Pro	Thr	Glu	
				220					225					230	235	
ctc	aat	gtg	cgc	cgg	cgt	ggg	gac	gcc	gtg	gag	gca	tgg	cga	ccc	gaa	773
Leu	Asn	Val	Arg	Arg	Arg	Gly	Asp	Ala	Val	Glu	Ala	Trp	Arg	Pro	Glu	

	240	245	250	
gac acc cag ctc gcc cgc ggt ggc act gcg acc gtg gaa gcc gtg acg				821
Asp Thr Gln Leu Ala Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr				
	255	260	265	
tat ttg ggc cgc gag tgg ctt gta caa acc acc gag ggg cac gcc gtg				869
Tyr Leu Gly Arg Glu Trp Leu Val Gln Thr Thr Glu Gly His Ala Val				
	270	275	280	
tcg gag gaa aaa ttc gac gtc ggc gaa agc gtc acg cta acc cag aag				917
Ser Glu Glu Lys Phe Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys				
	285	290	295	
aag gtg ttt agt ttc tagccgcctg caaaaggagg gag				955
Lys Val Phe Ser Phe				
300				

&lt;210&gt; 336

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 336

Met Ala Asp Leu Ser Ile Glu His Val Ser Arg Phe Phe Gly Asp Ala				
1	5	10	15	
Ile Ala Leu Asn Asp Val Ser Leu Thr Val Pro Ser Gly Ser Ile Thr				
	20	25	30	
Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr Thr Leu Leu Arg Leu				
	35	40	45	
Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr Val Ser Ile Gly Asn				
	50	55	60	
Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys Phe Gln Asp Ser Pro				
	65	70	75	80
Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val Ala Phe Pro Leu Lys				
	85	90	95	
Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val Lys Lys Arg Val Ser				
	100	105	110	
Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu Ala Arg Arg Lys Ile				
	115	120	125	
Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala				
	130	135	140	
Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp Glu Pro Met Ala His				
	145	150	155	160
Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala Asp Leu Arg Lys Ile				
	165	170	175	
Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val Thr His Ser Lys Ser				
	180	185	190	



<400> 337																	
atg	gca	ctg	ctg	atc	ctc	gcc	ggt	ctg	caa	atg	atc	ccg	aag	gaa	acc	48	
Met	Ala	Leu	Leu	Ile	Leu	Ala	Gly	Leu	Gln	Met	Ile	Pro	Lys	Glu	Thr		
1				5				10				15					
tac	gaa	gca	gcc	cgc	gtc	gat	ggc	gca	acc	gcg	tgg	cag	caa	ttc	acc	96	
Tyr	Glu	Ala	Ala	Arg	Val	Asp	Gly	Ala	Thr	Ala	Trp	Gln	Gln	Phe	Thr		
20				25				30									
aag	atc	acc	ctc	cgc	ctg	gtg	cgc	cca	gct	ttg	atg	gtg	gca	gta	ctc	144	
Lys	Ile	Thr	Leu	Pro	Leu	Val	Arg	Pro	Ala	Leu	Met	Val	Ala	Val	Leu		
35				40				45									
ttc	cgc	acc	ctc	gat	gcg	cta	cgc	atg	tat	gac	ctc	ccc	gtc	atc	atg	192	
Phe	Arg	Thr	Leu	Asp	Ala	Leu	Arg	Met	Tyr	Asp	Leu	Pro	Val	Ile	Met		
50				55				60									
atc	tcc	agc	tcc	tcc	aac	tcc	ccc	acc	gct	gtt	atc	tcc	cag	ctg	gtt	240	
Ile	Ser	Ser	Ser	Ser	Asn	Ser	Pro	Thr	Ala	Val	Ile	Ser	Gln	Leu	Val		
65				70				75				80					
gtg	gaa	gac	atg	cgc	caa	aac	aac	ttc	aac	tcc	gct	tcc	gcc	ctt	tcc	288	
Val	Glu	Asp	Met	Arg	Gln	Asn	Asn	Phe	Asn	Ser	Ala	Ser	Ala	Leu	Ser		
85				90				95									
aca	ctg	atc	ttc	ctg	ctg	atc	ttc	ttc	gtg	gcg	ttc	atc	atg	atc	cga	336	
Thr	Leu	Ile	Phe	Leu	Leu	Ile	Phe	Phe	Val	Ala	Phe	Ile	Met	Ile	Arg		
100				105				110									

ttc ctc ggc gca gat gtt tcg ggc caa cgc gga ata aag aaa aag aaa 384  
 Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys  
           115  125

ctg ggc gga acc aag gat gag aaa ccc acc gct aag gat gct gtt gta 432  
 Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val  
           130  140

aag gcc gat tct gct gtg aag gaa gcc gct aag cca tgactaaacg 478  
 Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro  
           145  155

aacaaaagga ctc 491

<210> 338

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ala Leu Leu Ile Leu Ala Gly Leu Gln Met Ile Pro Lys Glu Thr  
           1  10  15

Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr  
   20  25  30

Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu  
   35  40  45

Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met  
   50  55  60

Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val  
           65  70  75  80

Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser  
   85  90  95

Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg  
   100  105  110

Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys  
   115  120  125

Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val  
           130  135  140

Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro  
           145  150  155

<210> 339

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01297

&lt;400&gt; 339

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agaaatgatc tcgactgata gaaacgtttt ggtcaaaatc atg ggc tat gtc ggc 115  
Met Gly Tyr Val Gly  
1 5

atg gtt ctt gcc atc ttg ttc att ggc ctt ccg ctg gta ttt att gtg 163  
Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro Leu Val Phe Ile Val  
10 15 20

ctg act agc ttc aag cag cag tca gag att tac acc cag ccg gtc acg 211  
Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr Thr Gln Pro Val Thr  
25 30 35

tgg ttc cct tcg gaa ttt aat ttc gat aac tat gca aat gtt ttc gag 259  
Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr Ala Asn Val Phe Glu  
40 45 50

cgg gtt ccg ttc ctg aac tac ttc cgc aac tcg atc atc atc acg gtt 307  
Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser Ile Ile Ile Thr Val  
55 60 65

att ttg tgt ctg gtg aag att atc ttg ggt gtg atc tct gca tat gcg 355  
Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val Ile Ser Ala Tyr Ala  
70 75 80 85

ttg tcg att ttg cgc ttc ccg ggt cga aac ctt gtg ttc ttg ctg gtt 403  
Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu Val Phe Leu Leu Val  
90 95 100

atc tcc gcg ctg atg gtg cct tcc gaa gtg act gtt att tcc aac tat 451  
Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr Val Ile Ser Asn Tyr  
105 110 115

gcg ttg gtc agt cag ctt ggt tgg cgc gat acc tac cag ggc atc atc 499  
Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr Tyr Gln Gly Ile Ile  
120 125 130

gtt ccg cta gcg ggt att gct ttc gga acg ttc ctc atg cgt aac cac 547  
Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe Leu Met Arg Asn His  
135 140 145

ttc atg tct att cct tct gag ctc att gaa gct gcg cga atg gat cac 595  
Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala Ala Arg Met Asp His  
150 155 160 165

tgt gga cac ttc agg ttg ctc tgg aag gtt ttg ctt cca atc tct atg 643  
Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu Leu Pro Ile Ser Met  
170 175 180

cct acg ttg gtg gcg ttc tcc atg atc acc gtg gtg aat gaa tgg aac 691  
Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val Val Asn Glu Trp Asn  
185 190 195

caa tac ctg tgg cct ttc ctg atg gca gaa acc gat aat tca gca act 739  
Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr Asp Asn Ser Ala Thr  
200 205 210

ctg ccc att ggt ttg acc atg ctt caa aac aat gag ggt gtc tcc aac 787

Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn Glu Gly Val Ser Asn  
 215 220 225  
 tgg gga cct gtc atg gcc gca acg atc atg acc atg ttg cct gtg ctt 835  
 Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr Met Leu Pro Val Leu  
 230 235 240 245  
 gtg atg ttc ttg gca ctg cag gag tac atg atc aag gga ctt atc tcc 883  
 Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile Lys Gly Leu Ile Ser  
 250 255 260  
 ggc gcc gtc aag ggc taaaaacttc tcgctaaaaa ctt 921  
 Gly Ala Val Lys Gly  
 265

<210> 340  
 <211> 266  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 340  
 Met Gly Tyr Val Gly Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro  
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 Leu Val Phe Ile Val Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr  
 20 25 30  
 Thr Gln Pro Val Thr Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr  
 35 40 45  
 Ala Asn Val Phe Glu Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser  
 50 55 60  
 Ile Ile Ile Thr Val Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val  
 65 70 75 80  
 Ile Ser Ala Tyr Ala Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu  
 85 90 95  
 Val Phe Leu Leu Val Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr  
 100 105 110  
 Val Ile Ser Asn Tyr Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr  
 115 120 125  
 Tyr Gln Gly Ile Ile Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe  
 130 135 140  
 Leu Met Arg Asn His Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala  
 145 150 155 160  
 Ala Arg Met Asp His Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu  
 165 170 175  
 Leu Pro Ile Ser Met Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val  
 180 185 190  
 Val Asn Glu Trp Asn Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr  
 195 200 205

Asp Asn Ser Ala Thr Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn  
 210 215 220

Glu Gly Val Ser Asn Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr  
 225 230 235 240

Met Leu Pro Val Leu Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile  
 245 250 255

Lys Gly Leu Ile Ser Gly Ala Val Lys Gly  
 260 265

<210> 341  
 <211> 899  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(876)  
 <223> RXS00088

<400> 341

atc gaa gac aac cac ggc acc gaa ggg atc tcc ctg cca atc gag ggc	48
Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly	
1 5 10 15	
gtc gct gcg acc gac aac cgc gca ttc gaa ctg ctt gat cgc tgg ggt	96
Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly	
20 25 30	
gta gag ctg gtt gca gct cca ctt cag ctg gtt cca ttt acc gtt acg	144
Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr	
35 40 45	
ggc tac acc gaa gag ggc ggc gtc gct aac ctt ggc tcc cac cgc gag	192
Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu	
50 55 60	
cca gac ctg gaa gca ctt gct gct gca cag cct tcc ctg atc atc aac	240
Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn	
65 70 75 80	
ggc cag cgc ttc gct cag tac tac gat gac atc att gcc ctg aac cct	288
Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro	
85 90 95	
gac gca acc gtt gtt gag cta gac cca cgc gat ggc gag cca ctt gac	336
Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp	
100 105 110	
cag gag ctt atc cgc cag gct gaa acc ctg ggt gag atc ttc ggc gaa	384
Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu	
115 120 125	
gaa gaa gat gct gca aag atc gtt gct gat ttc gag tcc gca ctt gag	432
Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu	
130 135 140	
cgc gct aag acc gca tac gca gca atc tcc gac cag acc gtc atg gca	480

Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala  
 145 150 155 160  
 gtt aac gtt tcc ggc gga aac att ggc tac atc gct cct tcc gtt gga 528  
 Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly  
 165 170 175  
 cgc acc tac ggt cca atc ttc gac ctg gtt gga ctc acc cca gca ctc 576  
 Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu  
 180 185 190  
 gag gtt ggc aac gcg tcc tcc gac cac gag ggc gac gac att aac gtc 624  
 Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val  
 195 200 205  
 gaa gca atc gca gct gca aac cca gac ctg atc ctg gtc atg gac cgc 672  
 Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg  
 210 215 220  
 gat ggt ggc acc agc acc cgc aac gaa gct gat tac gtt cca gca gag 720  
 Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu  
 225 230 235 240  
 cag atc gtc tcc gac aat gaa gca ctg gca aac gtc aag gct gtc acc 768  
 Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr  
 245 250 255  
 gac gga tac gtt tac tac gca cct gca gat acc tac acc aac gaa aac 816  
 Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn  
 260 265 270  
 atc atc acc tac acc gag atc ctc aac ggc atg gca gat atg ttc gag 864  
 Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu  
 275 280 285  
 aag gca gct cag taggggatcg atccacact gac 899  
 Lys Ala Ala Gln  
 290

&lt;210&gt; 342

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 342

Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly  
 1 5 10 15  
 Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly  
 20 25 30  
 Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr  
 35 40 45  
 Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu  
 50 55 60  
 Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn  
 65 70 75 80

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<210> 343
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1177)
<223> RXS00372
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<400> 343
gcagacatTTT ccataagTcc tgcgaaatgc gcccatTCat gtaaagatgt tatttcctcc 60

cccaaact ccttaaaatt tcaagaagg ccttatttttc atg tct tcg aag cac 115
                                         Met Ser Ser Lys His
                                         1                               5

cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163

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Pro	Leu	Lys	Arg	Thr	Ala	Val	Thr	Val	Phe	Ala	Leu	Gly	Ala	Ser	Ala		
				10					15					20			
gct	ctc	ctc	gtg	gct	tgc	tct	gaa	cct	tct	gag	gac	gtt	tcc	acc	gca	211	
Ala	Leu	Leu	Val	Ala	Cys	Ser	Glu	Pro	Ser	Glu	Asp	Val	Ser	Thr	Ala		
			25					30					35				
gag	acc	acc	act	gca	agc	tct	tcc	gct	aac	gca	tcc	gat	gca	gcc	ggt	259	
Glu	Thr	Thr	Thr	Ala	Ser	Ser	Ser	Ala	Asn	Ala	Ser	Asp	Ala	Ala	Gly		
			40					45					50				
gaa	aaa	gta	acc	atc	acc	gtc	tac	acc	tct	gag	cct	gag	gaa	aag	gtc	307	
Glu	Lys	Val	Thr	Ile	Thr	Val	Tyr	Thr	Ser	Glu	Pro	Glu	Glu	Lys	Val		
	55						60					65					
gat	gag	atc	aac	aag	gcg	ttc	atg	gaa	gcc	aac	cca	gat	att	gag	gtt	355	
Asp	Glu	Ile	Asn	Lys		Phe	Met	Glu	Ala	Asn	Pro	Asp	Ile	Glu	Val		
	70					75				80					85		
gag	gtg	tac	cgc	gct	ggt	act	ggc	gat	ctg	act	gct	cgc	att	gaa	gct	403	
Glu	Val	Tyr	Arg	Ala	Gly	Thr	Gly	Asp	Leu	Thr	Ala	Arg	Ile	Glu	Ala		
				90					95					100			
gaa	aag	gca	tcc	ggt	tct	atc	gag	gct	gat	gtg	ttg	tgg	gct	gcg	gat	451	
Glu	Lys	Ala	Ser	Gly	Ser	Ile	Glu	Ala	Asp	Val	Leu	Trp	Ala	Ala	Asp		
			105					110					115				
gct	gca	acc	ttt	gaa	act	tat	gca	gca	cag	ggc	gac	ctt	gca	gag	ctg	499	
Ala	Ala	Thr	Phe	Glu	Thr	Tyr	Ala	Ala	Gln	Gly	Asp	Leu	Ala	Glu	Leu		
			120					125					130				
gaa	gat	gtt	gag	act	tcc	gac	atc	att	gaa	gag	gct	ctg	gat	gct	gag	547	
Glu	Asp	Val	Glu	Thr	Ser	Asp	Ile	Ile	Glu	Glu	Ala	Leu	Asp	Ala	Glu		
	135					140					145						
aac	ttt	tat	gta	ggc	acc	cgc	atc	atc	cca	acc	gtg	att	gca	tac	aac	595	
Asn	Phe	Tyr	Val	Gly	Thr	Arg	Ile	Ile	Pro	Thr	Val	Ile	Ala	Tyr	Asn		
	150					155					160				165		
act	gaa	gtt	gtt	gat	cag	gct	gag	ctt	cct	acg	tct	tgg	gct	gat	ctg	643	
Thr	Glu	Val	Val	Asp	Gln	Ala	Glu	Leu	Pro	Thr	Ser	Trp	Ala	Asp	Leu		
				170					175					180			
act	gat	cct	aag	tat	gca	ggc	caa	ctg	gtc	atg	ccg	gat	cca	gct	gtg	691	
Thr	Asp	Pro	Lys	Tyr	Ala	Gly	Gln	Leu	Val	Met	Pro	Asp	Pro	Ala	Val		
			185					190					195				
tct	ggt	gct	gca	gcc	ttc	aat	gct	tct	gtg	tgg	aag	aac	gac	cct	gcg	739	
Ser	Gly	Ala	Ala	Ala	Phe	Asn	Ala	Ser	Val	Trp	Lys	Asn	Asp	Pro	Ala		
		200					205						210				
ctt	ggc	gaa	gcc	tgg	atc	acc	gcc	ttg	ggt	gaa	aac	caa	cca	atg	atc	787	
Leu	Gly	Glu	Ala	Trp	Ile	Thr	Ala	Leu	Gly	Glu	Asn	Gln	Pro	Met	Ile		
		215					220					225					
gct	cag	tcc	aac	ggc	cca	acc	tcc	cag	gag	atc	gct	ggc	ggt	ggc	cac	835	
Ala	Gln	Ser	Asn	Gly	Pro	Thr	Ser	Gln	Glu	Ile	Ala	Gly	Gly	Gly	His		
	230					235				240					245		
cca	gtg	ggc	atc	gtg	gtg	gac	tac	ttg	gtg	cgc	gac	ttg	gct	gct	gct	883	
Pro	Val	Gly	Ile	Val	Val	Asp	Tyr	Leu	Val	Arg	Asp	Leu	Ala	Ala	Ala		



250										255					260					
gga tct cca atc gac acc atc tac gca tgc gag ggt tct cct tac atc	931																			
Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile																				
265	270	275																		
act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc	979																			
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala																				
280	285	290																		
gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca	1027																			
Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala																				
295	300	305																		
gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag	1075																			
Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu																				
310	315	320	325																	
ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag	1123																			
Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu																				
330	335	340																		
gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca	1171																			
Val Val Thr Ala Asp Lys Ala Ala Val Glu Phe Phe Gln Asn Ala																				
345	350	355																		
atg aac tagttttcct atgcagttat ctc	1200																			
Met Asn																				

&lt;210&gt; 344

&lt;211&gt; 359

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 344

Met Ser Ser Lys His Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala	
1 5 10 15	
Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu	
20 25 30	
Asp Val Ser Thr Ala Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala	
35 40 45	
Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu	
50 55 60	
Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn	
65 70 75 80	
Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr	
85 90 95	
Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val	
100 105 110	
Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly	
115 120 125	

Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu  
 130 135 140  
 Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr  
 145 150 155 160  
 Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr  
 165 170 175  
 Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met  
 180 185 190  
 Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp  
 195 200 205  
 Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu  
 210 215 220  
 Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile  
 225 230 235 240  
 Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg  
 245 250 255  
 Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu  
 260 265 270  
 Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu  
 275 280 285  
 Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu  
 290 295 300  
 Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp  
 305 310 315 320  
 Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met  
 325 330 335  
 Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu  
 340 345 350  
 Phe Phe Gln Asn Ala Met Asn  
 355

<210> 345  
 <211> 1059  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1036)  
 <223> RXS02590

<400> 345  
 gccccaaagg cttaaagtaa tgggcatgcc cactccttct tcgaccaaaa gctacgctgc 60  
 ggtcttacct ccacctggcc cctcgtgggc tggttccctc atg ggc atc tca ttg 115  
 Met Gly Ile Ser Leu

	1	5	
ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc			163
Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe	10	20	
ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg			211
Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp	25	35	
cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg			259
Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu Val Met Pro Ala Trp	40	50	
gca atg ctg tcc atg ggt ttg atc gca ttg gga act gca agc ccc gta			307
Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly Thr Ala Ser Pro Val	55	65	
gtt ttg ggt gat gat ctg tgg gga ttt atg ttt gtg tgc tgg tct att			355
Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe Val Cys Trp Ser Ile	70	80	85
ggc aca gcc gtg gga ctt gtt gcc tat tcc tta tat ata acg gcc att			403
Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu Tyr Ile Thr Ala Ile	90	95	100
ttg cga tct aag gcg ggc aca cca act ttt gcg tgg ggt ctt cct ctt			451
Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala Trp Gly Leu Pro Leu	105	110	115
gtc acg ccg atg gtt gct tcc acc tcg gca gca caa ctc cat gag cac			499
Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala Gln Leu His Glu His	120	125	130
ttt gaa ctt ccg gcg atg ctg tgg gtt tct ttc ggg ctc ttc ctt tta			547
Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe Gly Leu Phe Leu Leu	135	140	145
act ttg gcg tct gca cca gca gtt ttt acc cga gtg tat ttc tac tat			595
Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg Val Tyr Phe Tyr Tyr	150	155	160
ttc ggc ccc aag gcg cag ggc atc cca ctg atg gca aca cca aca tca			643
Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met Ala Thr Pro Thr Ser	170	175	180
tgg att cct ttg ggt atg gtg ggc caa tcc act gca gca gct cag ctc			691
Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr Ala Ala Ala Gln Leu	185	190	195
atc ggt gcg tcc ttt gga tcc aag aca gca atc aca atg ggc att att			739
Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile Thr Met Gly Ile Ile	200	205	210
tac ggc atc atc atg gga att ttt acg att cct ctg gga gcc atc gct			787
Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro Leu Gly Ala Ile Ala	215	220	225
cac ttt gtg ttc tac aga gct gtt ttc aaa ggg gcg aca tac agc ccc			835
His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly Ala Thr Tyr Ser Pro	230	235	240
			245

Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met  
165 170 175

Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr  
180 185 190

Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile  
195 200 205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro  
210 215 220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly  
225 230 235 240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr  
245 250 255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp  
260 265 270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val  
275 280 285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val  
290 295 300

Gly Lys Leu Lys Ser Gln Leu Ala  
305 310

<210> 347

<211> 1725

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1702)

<223> RXS00758

<400> 347

ttcaagtttg gctgtgactc atgtcgacata tagtattttca atcaccggat ccgcacgatt 60

gcaaaatcct ggggaatatt cataacaacg gaggtcactc atg act ttg aag aag 115  
Met Thr Leu Lys Lys  
1 5

tct ctc gct gta acc acg gcg gct gca ctt gct ttg agc ctt gcc gct 163  
Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala Leu Ser Leu Ala Ala  
10 15 20

tgc tgc tcc gac tcc tcg tcc gac agc tcc tca tcc tca tca ggc agc 211  
Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Gly Ser  
25 30 35

gaa ggc ggc gac aac tac gtc ctc gtc aac ggc act gag cca cag aac 259  
Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly Thr Glu Pro Gln Asn  
40 45 50

ccg ctc gtc cca ggc aac acc aac gaa gta ggt ggc ggt cgc atc gtc 307  
Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly Gly Gly Arg Ile Val  
55 60 65

gac agc atc ttc tcc ggc ctg gtc tac tac gac gtc gac ggc tcc cct 355  
 Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp Val Asp Gly Ser Pro  
 70 75 80 85

gtc aac gat gtt gca gag tcc atc gaa ctc gaa ggt gac aag acc tac 403  
 Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu Gly Asp Lys Thr Tyr  
 90 95 100

cgc atc acc atc aaa gac ggc cag acc ttc acc gat ggc acc cca gtt 451  
 Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr Asp Gly Thr Pro Val  
 105 110 115

acc gct gag agc ttt gtc aac gca tgg aac tac aac gta gct aac agc 499  
 Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr Asn Val Ala Asn Ser  
 120 125 130

acg ctg tcc tcc tac ttc ttt gag tcc atc ctc ggc tac gaa gaa ggc 547  
 Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu Gly Tyr Glu Glu Gly  
 135 140 145

gtc gag tcc atg gaa ggc ctc cag gtc gtc gac gac acc acc ttc acc 595  
 Val Glu Ser Met Glu Gly Leu Gln Val Val Asp Asp Thr Thr Phe Thr  
 150 155 160 165

gtc gag ctc acc cag cct gag tcc gac ttc cca ctg cgc ctg gga tac 643  
 Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro Leu Arg Leu Gly Tyr  
 170 175 180

tcc gca ttc ttc ccg ctt cct gaa tcc gca ttt gac gac atg gac gca 691  
 Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe Asp Asp Met Asp Ala  
 185 190 195

ttc ggt gag aac cca atc ggc aac ggt cca tac aag ctc caa gag tgg 739  
 Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr Lys Leu Gln Glu Trp  
 200 205 210

aac cac aac cag gac gcc acc atc gtt cct aac gcg gac tac acc ggt 787  
 Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn Ala Asp Tyr Thr Gly  
 215 220 225

gga cgc cag gct cag aac gac ggc gtg aag ttc atc ttc tac cca acc 835  
 Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe Ile Phe Tyr Pro Thr  
 230 235 240 245

ttc gac tcc gct tac gcg gac ctg ctc tcc gac aac ttg gat gtg ctg 883  
 Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp Asn Leu Asp Val Leu  
 250 255 260

gac gct atc cca gac tcc gcg ttc tcc tcc ttc gag gac gag ctc tct 931  
 Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe Glu Asp Glu Leu Ser  
 265 270 275

ggc cgt tcc atc aac cag cct tcc gct gtg ttc cag tcc ttc acc atc 979  
 Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe Gln Ser Phe Thr Ile  
 280 285 290

ccg gag agc ctt gag cac ttc tcc ggc gaa gaa ggc gtg ctg cgt cgc 1027  
 Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu Gly Val Leu Arg Arg  
 295 300 305

cag gcc atc tcc ttg gcc gtc aac cgc gac gag atc acc caa acc atc 1075

Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu Ile Thr Gln Thr Ile  
 310 315 320 325  
 ttc gaa ggc acc cgc acc cca gcg acg gac ttc acc tcc cct gtc atc 1123  
 Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe Thr Ser Pro Val Ile  
 330 335 340  
 gac gga cac tct gat tcc ctc cag ggc gca gat gtc ttg acc tac gat 1171  
 Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp Val Leu Thr Tyr Asp  
 345 350 355  
 cca gag cgc gct cag gaa ctg tgg gca cag gca gac gag atc agc cct 1219  
 Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala Asp Glu Ile Ser Pro  
 360 365 370  
 tgg tcc ggc gag ttc tcc atc tcc tac aac gca gac ggt gga cac cag 1267  
 Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala Asp Gly Gly His Gln  
 375 380 385  
 gca tgg gtg gac gca acc gcc aat tcc atc cgc aac acc ctg ggt atc 1315  
 Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg Asn Thr Leu Gly Ile  
 390 395 400 405  
 gac gcc atc ggc aac cca tac cca gac ttc aag tcc ctg cgt gac gat 1363  
 Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys Ser Leu Arg Asp Asp  
 410 415 420  
 gtc acc aac cgc acc atc aac ggc gca ttc cgc acc ggc tgg cag gca 1411  
 Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg Thr Gly Trp Gln Ala  
 425 430 435  
 gac tac cgc tcc ttg ggc aac ttc ctc gga cct ttg tac ggc acc ggt 1459  
 Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro Leu Tyr Gly Thr Gly  
 440 445 450  
 gca ggc tcc aac gat ggt gac tac tcc aac cca gat ttc gat gcc aag 1507  
 Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro Asp Phe Asp Ala Lys  
 455 460 465  
 ctc gcc gaa gca gca aac gcg gcc gat gtt gac gca tca acc ccg cta 1555  
 Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp Ala Ser Thr Pro Leu  
 470 475 480 485  
 tac aac gaa gca cag gaa atc ctg ctc cag gat ctc cca gcg atc cca 1603  
 Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp Leu Pro Ala Ile Pro  
 490 495 500  
 act tgg tac tcc aac gca gtt ggt gga tac tcc acc aac gtg gac aac 1651  
 Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser Thr Asn Val Asp Asn  
 505 510 515  
 gtg gaa ttc cag tgg aac tcg caa cct gcg tac tac cag atc acc aag 1699  
 Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr Tyr Gln Ile Thr Lys  
 520 525 530  
 aac tagtagcttc gcaccacccg ctc  
 Asn 1725

<211> 534  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 348

Met Thr Leu Lys Lys Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala  
1 5 10 15

Leu Ser Leu Ala Ala Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser  
20 25 30

Ser Ser Ser Gly Ser Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly  
35 40 45

Thr Glu Pro Gln Asn Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly  
50 55 60

Gly Gly Arg Ile Val Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp  
65 70 75 80

Val Asp Gly Ser Pro Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu  
85 90 95

Gly Asp Lys Thr Tyr Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr  
100 105 110

Asp Gly Thr Pro Val Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr  
115 120 125

Asn Val Ala Asn Ser Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu  
130 135 140

Gly Tyr Glu Glu Gly Val Glu Ser Met Glu Gly Leu Gln Val Val Asp  
145 150 155 160

Asp Thr Thr Phe Thr Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro  
165 170 175

Leu Arg Leu Gly Tyr Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe  
180 185 190

Asp Asp Met Asp Ala Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr  
195 200 205

Lys Leu Gln Glu Trp Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn  
210 215 220

Ala Asp Tyr Thr Gly Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe  
225 230 235 240

Ile Phe Tyr Pro Thr Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp  
245 250 255

Asn Leu Asp Val Leu Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe  
260 265 270

Glu Asp Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe  
275 280 285

Gln Ser Phe Thr Ile Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu  
290 295 300



Gly Val Leu Arg Arg Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu  
 305 310 315 320  
 Ile Thr Gln Thr Ile Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe  
 325 330 335  
 Thr Ser Pro Val Ile Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp  
 340 345 350  
 Val Leu Thr Tyr Asp Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala  
 355 360 365  
 Asp Glu Ile Ser Pro Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala  
 370 375 380  
 Asp Gly Gly His Gln Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg  
 385 390 395 400  
 Asn Thr Leu Gly Ile Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys  
 405 410 415  
 Ser Leu Arg Asp Asp Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg  
 420 425 430  
 Thr Gly Trp Gln Ala Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro  
 435 440 445  
 Leu Tyr Gly Thr Gly Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro  
 450 455 460  
 Asp Phe Asp Ala Lys Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp  
 465 470 475 480  
 Ala Ser Thr Pro Leu Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp  
 485 490 495  
 Leu Pro Ala Ile Pro Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser  
 500 505 510  
 Thr Asn Val Asp Asn Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr  
 515 520 525  
 Tyr Gln Ile Thr Lys Asn  
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<210> 349

<211> 1698

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1675)

<223> RXS01346

<400> 349

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ggcacgttgc aaacagcaac gctcacccat aggagattta atg cgc aca gcc aca 115

	Met	Arg	Thr	Ala	Thr	
	1				5	
aaa gtc atc gca aca gtg atg gcc tca acc ctg gct atc ggg ctg gca						163
Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu Ala Ile Gly Leu Ala						
	10				20	
tct tgt tcc agc tct agt ggc acc cca gac gtg aat tac gta tcc gtc						211
Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val Asn Tyr Val Ser Val						
	25				35	
aac ggc acc gaa cct cag cgc gga ctc atc ccg ggc gac acc aat gaa						259
Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro Gly Asp Thr Asn Glu						
	40				50	
aac ggc ggt ggg cga gtg gtg gac atg ctg tac tct ggg ctc gtc tac						307
Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr Ser Gly Leu Val Tyr						
	55				65	
ttt gat gaa gct ggc gtt gct caa aat gac ctg gcg gca tca att gac						355
Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu Ala Ala Ser Ile Asp						
	70				80	85
cag gaa aca gac acc acc tac aaa atc act ttg cgt gat ggc atc aaa						403
Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu Arg Asp Gly Ile Lys						
	90				95	100
ttc agt gac gga tgc gat att act gcc act gat ttt gtg gat acc tgg						451
Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp Phe Val Asp Thr Trp						
	105				110	115
aat ttt gta gtg gaa aat gga ctg ctc aac act tct ttc ttc tca ccg						499
Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr Ser Phe Phe Ser Pro						
	120				125	130
att aaa ggg tat gag gag ggc gtg gaa acg ctc gag ggt ttg aat gtg						547
Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu Glu Gly Leu Asn Val						
	135				140	145
gtg gat gat cgc aca ttt acc atc gag ctt gcc caa ccg gat tct gag						595
Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala Gln Pro Asp Ser Glu						
	150				160	165
ttc acc caa cgc att ggc tac tac ggt ttt gca ccg atg cca gct tgc						643
Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala Pro Met Pro Ala Ser						
	170				175	180
gct cgc gat gat att gac gcc ttt ggt gaa aac ccc gtg tcc tct ggc						691
Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn Pro Val Ser Ser Gly						
	185				190	195
cct tac aaa cta gag cag tgg gat cac aac gca gaa ctg aaa gtg gtg						739
Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala Glu Leu Lys Val Val						
	200				205	210
gcc aat gaa cac tac gat ggc ccg cgc gca gcc aac aac gat ggc ttg						787
Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala Asn Asn Asp Gly Leu						
	215				220	225
aag tac gtg ttc tac gcc caa aat gat gca gct tat tca gat ctg ttg						835
Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala Tyr Ser Asp Leu Leu						

230	235	240	245	
gct gga aac cta gat	gtg ctg gat ctc att	cca cca tcg gcg tac acc		883
Ala Gly Asn Leu Asp	Val Leu Asp Leu Ile	Pro Pro Ser Ala Tyr Thr		
250	255	260		
acc tat gaa gag gaa	ctg tcg ggt cga tcc att	aat caa cct gcg gcc		931
Thr Tyr Glu Glu Glu	Leu Ser Gly Arg Ser Ile	Asn Gln Pro Ala Ala		
265	270	275		
tcc tat ctg gaa ctc	tcc att cgc atg gaa tcc	ccc aac ttt gaa ggg		979
Ser Tyr Leu Glu Leu	Ser Ile Arg Met Glu Ser	Pro Asn Phe Glu Gly		
280	285	290		
caa cag gga cag ttg	cgt cga caa gca att tct	atg gcg att aac cgt		1027
Gln Gln Gly Gln Leu	Arg Arg Gln Ala Ile Ser	Met Ala Ile Asn Arg		
295	300	305		
gaa gaa atc gct gag	cag atc ttc gcc ggc acc	tac acg cct gcg ctc		1075
Glu Glu Ile Ala Glu	Gln Ile Phe Ala Gly Thr	Tyr Thr Pro Ala Leu		
310	315	320	325	
gac ttc acc gcg ccc	gtg ctc gac ggc tgg	cgc gat gat ttg aac ggc		1123
Asp Phe Thr Ala Pro	Val Leu Asp Gly Trp Arg	Asp Asp Leu Asn Gly		
330	335	340		
aat gac gtg ctg act	ttc cag cct gac aag gcc	cggt gag ctg tgg gaa		1171
Asn Asp Val Leu Thr	Phe Gln Pro Asp Lys Ala	Arg Glu Leu Trp Glu		
345	350	355		
gac gct gag gag atc	gca cct ttt gag ggc gaa	ttg cag atc agt tac		1219
Asp Ala Glu Glu Ile	Ala Pro Phe Glu Gly Glu	Leu Gln Ile Ser Tyr		
360	365	370		
aac gcg gat gtt ccc	aac cgg gaa tgg gtg gat	gcg gta gca aac agc		1267
Asn Ala Asp Val Pro	Asn Arg Glu Trp Val Asp	Ala Val Ala Asn Ser		
375	380	385		
atc agc aac gaa tta	gac gtc aac gcc act ggc	aat cct ttc ccc gat		1315
Ile Ser Asn Glu Leu	Asp Val Asn Ala Thr Gly	Asn Pro Phe Pro Asp		
390	395	400	405	
ttt aaa tcc ttc cgc	gac aca tac cgc acc acc	gga ttg gat ggc gcc		1363
Phe Lys Ser Phe Arg	Asp Thr Tyr Arg Thr Thr	Gly Leu Asp Gly Ala		
410	415	420		
tac cgc acc gcg tgg	ttt gcg gac tac cca	agc atc ggc aac ttc ctt		1411
Tyr Arg Thr Ala Trp	Phe Ala Asp Tyr Pro	Ser Ile Gly Asn Phe Leu		
425	430	435		
gga cct aac tac acc	tcg ggc gtg gcc tcc	aac gat gcc aag tac gaa		1459
Gly Pro Asn Tyr Thr	Ser Gly Val Ala Ser Asn	Asp Ala Lys Tyr Glu		
440	445	450		
aac cca gaa ttt gat	caa ttg att gcc gac gcc	gca gca gcc tcc acc		1507
Asn Pro Glu Phe Asp	Gln Leu Ile Ala Asp Ala	Ala Ala Ala Ala Ser Thr		
455	460	465		
aag gag gaa acc ttc	cag gca tat gcg cag gcc	cag gaa atg ttg ttg		1555
Lys Glu Glu Thr Phe	Gln Ala Tyr Ala Gln Ala	Gln Glu Met Leu Leu		
470	475	480	485	

cgc gat ctt ccc gca atc cca ctg tgg tac ccg aat gtg gtt ggc ggc 1603  
 Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro Asn Val Val Gly Gly  
                   490                  495                  500

tac tca gaa tcc gtg gac aac gtc tcc gta aac tgg aag gcc ata cct 1651  
 Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn Trp Lys Ala Ile Pro  
                   505                  510                  515

gtt tat tgg gca att aca aag caa taaactcatt aacctaaatc cgg 1698  
 Val Tyr Trp Ala Ile Thr Lys Gln  
                   520                  525

<210> 350

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Met Arg Thr Ala Thr Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu  
   1                  5                  10                  15

Ala Ile Gly Leu Ala Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val  
                   20                  25                  30

Asn Tyr Val Ser Val Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro  
                   35                  40                  45

Gly Asp Thr Asn Glu Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr  
                   50                  55                  60

Ser Gly Leu Val Tyr Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu  
   65                  70                  75                  80

Ala Ala Ser Ile Asp Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu  
                   85                  90                  95

Arg Asp Gly Ile Lys Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp  
                   100                  105                  110

Phe Val Asp Thr Trp Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr  
                   115                  120                  125

Ser Phe Phe Ser Pro Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu  
   130                  135                  140

Glu Gly Leu Asn Val Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala  
   145                  150                  155                  160

Gln Pro Asp Ser Glu Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala  
                   165                  170                  175

Pro Met Pro Ala Ser Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn  
                   180                  185                  190

Pro Val Ser Ser Gly Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala  
                   195                  200                  205

Glu Leu Lys Val Val Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala  
   210                  215                  220

Asn Asn Asp Gly Leu Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala  
 225 230 235 240  
 Tyr Ser Asp Leu Leu Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro  
 245 250 255  
 Pro Ser Ala Tyr Thr Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile  
 260 265 270  
 Asn Gln Pro Ala Ala Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser  
 275 280 285  
 Pro Asn Phe Glu Gly Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser  
 290 295 300  
 Met Ala Ile Asn Arg Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr  
 305 310 315 320  
 Tyr Thr Pro Ala Leu Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg  
 325 330 335  
 Asp Asp Leu Asn Gly Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala  
 340 345 350  
 Arg Glu Leu Trp Glu Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu  
 355 360 365  
 Leu Gln Ile Ser Tyr Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp  
 370 375 380  
 Ala Val Ala Asn Ser Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly  
 385 390 395 400  
 Asn Pro Phe Pro Asp Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr  
 405 410 415  
 Gly Leu Asp Gly Ala Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser  
 420 425 430  
 Ile Gly Asn Phe Leu Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn  
 435 440 445  
 Asp Ala Lys Tyr Glu Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala  
 450 455 460  
 Ala Ala Ala Ser Thr Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala  
 465 470 475 480  
 Gln Glu Met Leu Leu Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro  
 485 490 495  
 Asn Val Val Gly Gly Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn  
 500 505 510  
 Trp Lys Ala Ile Pro Val Tyr Trp Ala Ile Thr Lys Gln  
 515 520 525

&lt;210&gt; 351

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)..(298)

&lt;223&gt; RXS00912

&lt;400&gt; 351

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ccacaccttt gaaaggagct aagcg atg gac aac acc ctc tac aca gca ggc      52
                        Met Asp Asn Thr Leu Tyr Thr Ala Gly
                          1                      5

ctc aca atc gca gct gcc ttt ttc atg ctg tcg ttc atc ttc acc atc      100
Leu Thr Ile Ala Ala Phe Phe Met Leu Ser Phe Ile Phe Thr Ile
  10                      15                      20                      25

tac cgc atc atc gtc ggg ccc aac tcc atc gat cgc cta ctc ggc ctg      148
Tyr Arg Ile Ile Val Gly Pro Asn Ser Ile Asp Arg Leu Leu Gly Leu
                      30                      35                      40

gac gga acc gtc tcc atg att caa tgc tcc atg gcc acc tac atc tgc      196
Asp Gly Thr Val Ser Met Ile Gln Cys Ser Met Ala Thr Tyr Ile Cys
          45                      50                      55

tgg aca ctc gac acc acc gtc acc aac ttc atg atg gtc atc gca ctc      244
Trp Thr Leu Asp Thr Thr Val Thr Asn Phe Met Met Val Ile Ala Leu
          60                      65                      70

tta gga ttc atc agc tct gta tcc gta gcc cgc ttc cgc aag agg gat      292
Leu Gly Phe Ile Ser Ser Val Ser Val Ala Arg Phe Arg Lys Arg Asp
          75                      80                      85

ggt gcc taaatgaccc tgcaactatt cac      321
Gly Ala
  90

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&lt;210&gt; 352

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 352

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Met Asp Asn Thr Leu Tyr Thr Ala Gly Leu Thr Ile Ala Ala Ala Phe
  1                      5                      10                      15

Phe Met Leu Ser Phe Ile Phe Thr Ile Tyr Arg Ile Ile Val Gly Pro
          20                      25                      30

Asn Ser Ile Asp Arg Leu Leu Gly Leu Asp Gly Thr Val Ser Met Ile
          35                      40                      45

Gln Cys Ser Met Ala Thr Tyr Ile Cys Trp Thr Leu Asp Thr Thr Val
          50                      55                      60

Thr Asn Phe Met Met Val Ile Ala Leu Leu Gly Phe Ile Ser Ser Val
          65                      70                      75                      80

Ser Val Ala Arg Phe Arg Lys Arg Asp Gly Ala
          85                      90

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<210> 353  
 <211> 2472  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2449)  
 <223> RXS00453

<400> 353

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attcaggttg gggcgatggt cctataatcg caagtggatt gtg att tcg gca tgg      115
                                   Val Ile Ser Ala Trp
                                   1          5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag      163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
                                   10          15          20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc      211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
                                   25          30          35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg      259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
                                   40          45          50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt      307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
                                   55          60          65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att      355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
                                   70          75          80          85

gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct      403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Glu Arg Phe Gly Asn Pro
                                   90          95          100

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc      451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
                                   105          110          115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg      499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
                                   120          125          130

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att      547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
                                   135          140          145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc      595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
                                   150          155          160          165

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc      643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala

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170	175	180	
ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu 185 190 195			691
atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly 200 205 210			739
tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val 215 220 225			787
ggc att ggt gcg ctg gca att gtg ctg gcc acg gcg ttt act gat ctc Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr Ala Phe Thr Asp Leu 230 235 240 245			835
aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly 250 255 260			883
att gac tac gcg ctg ttt att ttg tct agg tac cgt gcg gag tat aag Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr Arg Ala Glu Tyr Lys 265 270 275			931
cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly 280 285 290			979
agt gcg gtg gtg ttt gct ggc gcg acg gtg att atc gcg ctg gta gcc Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala 295 300 305			1027
ctc atc att gcg gat atc gga ttc ctc acg gcc atg ggt att tct gcg Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala 310 315 320 325			1075
gcg ttt acg gtg ttc gtg gct gtg ctc att gcg ttg acg ttt atc ccg Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro 330 335 340			1123
gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro 345 350 355			1171
gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu 360 365 370			1219
aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala 375 380 385			1267
ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr 390 395 400 405			1315
att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser 410 415 420			1363



aat att gat acc act cag cgt cag tct gct gat ttg atg gca gag ggc Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly 425 430 435	1411
ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His 440 445 450	1459
gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln 455 460 465	1507
gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala 470 475 480 485	1555
acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys 490 495 500	1603
aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile 505 510 515	1651
ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu 520 525 530	1699
atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly 535 540 545	1747
act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr 550 555 560 565	1795
gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly 570 575 580	1843
ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro 585 590 595	1891
ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly 600 605 610	1939
gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr 615 620 625	1987
cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr 630 635 640 645	2035
ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg 650 655 660	2083

gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac 2131  
 Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr  
 665 670 675

acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc 2179  
 Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg  
 680 685 690

gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt 2227  
 Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe  
 695 700 705

att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt 2275  
 Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly  
 710 715 720 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc 2323  
 Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro  
 730 735 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg 2371  
 Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp  
 745 750 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag 2419  
 Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu  
 760 765 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca 2469  
 Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg  
 775 780

gat 2472

<210> 354

<211> 783

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Val Ile Ser Ala Trp Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala  
 1 5 10 15

Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr  
 20 25 30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln  
 35 40 45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro  
 50 55 60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala  
 65 70 75 80

Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu  
 85 90 95

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val  
 100 105 110

Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys  
 115 120 125  
 Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr  
 130 135 140  
 Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys  
 145 150 155 160  
 His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly  
 165 170 175  
 Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile  
 180 185 190  
 Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu  
 195 200 205  
 Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr  
 210 215 220  
 Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr  
 225 230 235 240  
 Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile  
 245 250 255  
 Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr  
 260 265 270  
 Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala  
 275 280 285  
 Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile  
 290 295 300  
 Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala  
 305 310 315 320  
 Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala  
 325 330 335  
 Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe  
 340 345 350  
 Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr  
 355 360 365  
 Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys  
 370 375 380  
 Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly  
 385 390 395 400  
 Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro  
 405 410 415  
 Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp  
 420 425 430

Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val  
 435 440 445  
 Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro  
 450 455 460  
 Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln  
 465 470 475 480  
 Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser  
 485 490 495  
 Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe  
 500 505 510  
 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys  
 515 520 525  
 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile  
 530 535 540  
 Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val  
 545 550 555 560  
 Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu  
 565 570 575  
 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg  
 580 585 590  
 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val  
 595 600 605  
 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly  
 610 615 620  
 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe  
 625 630 635 640  
 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu  
 645 650 655  
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln  
 660 665 670  
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe  
 675 680 685  
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala  
 690 695 700  
 Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe  
 705 710 715 720  
 Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg  
 725 730 735  
 Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp  
 740 745 750  
 Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu

755

760

765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg  
 770 775 780

&lt;210&gt; 355

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(574)

&lt;223&gt; RXS00932

&lt;400&gt; 355

cccaattaat ttatgcactt cggtgaggtt actcaciaaag agtagcgtgc aaagcccagc 60

aataagggtga tgtttcaacg attaggttac ggtagggggcc atg acg cca cag aaa 115  
 Met Thr Pro Gln Lys  
 1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163  
 Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu  
 10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211  
 Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr  
 25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259  
 Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala  
 40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307  
 Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly  
 55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355  
 Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe  
 70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403  
 Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe  
 90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451  
 Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala  
 105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499  
 Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile  
 120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547  
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp  
 135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac atg 597  
 Pro Asp Ala Ile Ala Asn Thr Val Asp

150

155

&lt;210&gt; 356

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly  
 1 5 10 15

Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val  
 20 25 30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe  
 35 40 45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp  
 50 55 60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp  
 65 70 75 80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala  
 85 90 95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe  
 100 105 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu  
 115 120 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met  
 130 135 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp  
 145 150 155

&lt;210&gt; 357

&lt;211&gt; 2313

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2290)

&lt;223&gt; RXS00479

&lt;400&gt; 357

tagatcccaa ggctcaaaat ttattactta aacaagttga gcaactagcc agccgcaaat 60

cttagaacta acctttacgc cttaacgga agtgaatttg atg tct act agc atc 115  
 Met Ser Thr Ser Ile  
 1 5

aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163  
 Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile  
 10 15 20

ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc	211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val	
25 30 35	
ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag	259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln	
40 45 50	
acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag	307
Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln	
55 60 65	
ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg	355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met	
70 75 80 85	
gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa	403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu	
90 95 100	
gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc	451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser	
105 110 115	
cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc	499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro	
120 125 130	
ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag	547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu	
135 140 145	
acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga	595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly	
150 155 160 165	
ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat	643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp	
170 175 180	
ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc	691
Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val	
185 190 195	
atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt	739
Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser	
200 205 210	
ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag	787
Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys	
215 220 225	
tgg gac atc ctg ctg ctt tcg ggt cag act caa ggc atc ctc ttc att	835
Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile	
230 235 240 245	
ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt	883
Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg	
250 255 260	
ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg	931

Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly  
 265 270 275

aaa gcc atc cgg gca tgc gtg gaa ccc att ctt gcc tgc ggc agc act 979  
 Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr  
 280 285 290

gtt att gcg ggc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac 1027  
 Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn  
 295 300 305

tcc acg cta ggt cca gta gct tgc gtg ggc att att ttt gca atg ctt 1075  
 Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu  
 310 315 320 325

tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg 1123  
 Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val  
 330 335 340

gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg 1171  
 Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala  
 345 350 355

aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta 1219  
 Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu  
 360 365 370

gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt 1267  
 Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu  
 375 380 385

ctc ttg ggt gcg got ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc 1315  
 Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser  
 390 395 400 405

caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag 1363  
 Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln  
 410 415 420

gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att 1411  
 Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile  
 425 430 435

atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac 1459  
 Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn  
 440 445 450

aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct 1507  
 Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser  
 455 460 465

ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt 1555  
 Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly  
 470 475 480 485

aca gct cca ggc ccg gta gtt gta gaa ggg caa gtc ctt tta caa gca 1603  
 Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln Val Leu Leu Gln Ala  
 490 495 500

aca ctt gtc gaa gca cca gat tcc gaa gaa gct caa aaa gct att cgc 1651  
 Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala Gln Lys Ala Ile Arg



505	510	515	
agt atc cgc caa act ttt gca gat gaa aat ata tca gcg gta gta ggc Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly 520 525 530			1699
ggg gtc act gca act tcc gta gac act aac gat gcc tcc atc cat gac Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp 535 540 545			1747
cgc aac ctg atc atc cca att gta ttg ctg gtc att ttg gtt att ctc Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu 550 555 560 565			1795
atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr 570 575 580			1843
acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe 585 590 595			1891
aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr 600 605 610			1939
gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu 615 620 625			1987
gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly 630 635 640 645			2035
att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly 650 655 660			2083
gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu 665 670 675			2131
ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp 680 685 690			2179
acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile 695 700 705			2227
gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln 710 715 720 725			2275
aag cag cct cag cta tgacacacca aaattcgcct ctc Lys Gln Pro Gln Leu 730			2313

&lt;210&gt; 358

&lt;211&gt; 730

Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser  
290 295 300

Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile  
 305 310 315 320  
 Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe  
 325 330 335  
 Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro  
 340 345 350  
 Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser  
 355 360 365  
 Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser  
 370 375 380  
 Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys  
 385 390 395 400  
 Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala  
 405 410 415  
 Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly  
 420 425 430  
 Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala  
 435 440 445  
 Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser  
 450 455 460  
 Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val  
 465 470 475 480  
 Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln  
 485 490 495  
 Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala  
 500 505 510  
 Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile  
 515 520 525  
 Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp  
 530 535 540  
 Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val  
 545 550 555 560  
 Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu  
 565 570 575  
 Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val  
 580 585 590  
 Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro  
 595 600 605  
 Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp  
 610 615 620  
 Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His

625	630	635	640
Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val	645	650	655
Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr	660	665	670
Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe	675	680	685
Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala	690	695	700
Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser	705	710	715
Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu	725	730	

<210> 359  
 <211> 393  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(370)  
 <223> RXS02586

<400> 359  
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 gatgccacca tcatccgcat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115  
 Met His Leu Leu Arg  
 1 5  
 gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163  
 Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val  
 10 15 20  
 atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211  
 Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg  
 25 30 35  
 cgc ctg aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259  
 Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala  
 40 45 50  
 ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307  
 Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg  
 55 60 65  
 gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355  
 Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg  
 70 75 80 85  
 ctt gag gat cta gat taaatctatg cgaggatttt tca 393  
 Leu Glu Asp Leu Asp  
 90

<210> 360  
 <211> 90  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 360  
 Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys  
           1                  5                  10                  15  
 Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro  
                   20                  25                  30  
 Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His  
                   35                  40                  45  
 Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser  
           50                  55                  60  
 Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg  
           65                  70                  75                  80  
 Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp  
                   85                  90

<210> 361  
 <211> 2214  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2191)  
 <223> RXS02587

<400> 361  
 agcctggata acctgccaga cgggtggcgca tggctgcagc cgttccgccc tctgactgcc 60  
 ttgttatoca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg 115  
   Val Phe Ser Lys Trp  
   1                  5  
 ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc 163  
 Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile  
                                   10                  15                  20  
 gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211  
 Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp  
                   25                  30                  35  
 cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct 259  
 Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Thr Ala  
                   40                  45                  50  
 gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat 307  
 Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp  
           55                  60                  65  
 gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca 355

Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala	
70 75 80 85	
gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac	403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn	
90 95 100	
aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat	451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn	
105 110 115	
caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg	499
Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly	
120 125 130	
ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa	547
Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu	
135 140 145	
gat cag ctc cat ccg gac aac ctt gcc ggt ggc gtc acc act gag gtc	595
Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly Val Thr Thr Glu Val	
150 155 160 165	
gcg ggt gcc acc gct gta gcc gac gca ctc gat gag ggc atg gct ggc	643
Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp Glu Gly Met Ala Gly	
170 175 180	
gat att tca cgc gcc gaa gtt ttt gcg ctg cct ttc gtg gct atc ttg	691
Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro Phe Val Ala Ile Leu	
185 190 195	
ctg ctc atc gtg ttt ggc tca gtt gtt gcc gcg gcg atg cca ttg atc	739
Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala Ala Met Pro Leu Ile	
200 205 210	
gtg ggc att ttg tcc atc ttg ggt tcg ctg ggc atc ttg gca att ttg	787
Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly Ile Leu Ala Ile Leu	
215 220 225	
gct gga ttc ttc cag gtc aac gta ttt gca caa tct gtt gtg acc ctt	835
Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln Ser Val Val Thr Leu	
230 235 240 245	
ctg ggc ttg ggt ctt gcc att gac tat ggc tta ttc atg gtc tct cgt	883
Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu Phe Met Val Ser Arg	
250 255 260	
ttc cgt gag gaa atg gat aag ggc acc ccg gtt gaa cag gct gtt gcc	931
Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val Glu Gln Ala Val Ala	
265 270 275	
acc act acg gcg acc gcg ggt aag act gtg gtg ttc tct gca gcg atg	979
Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val Phe Ser Ala Ala Met	
280 285 290	
gtg gct gtg gcg ctg tcc ggg ttg ttt gtt ttc cca cag gct ttc ttg	1027
Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe Pro Gln Ala Phe Leu	
295 300 305	
aag tcg gtg gca ttc ggt gcg att tcc gcg gtt ggc ctt gct gct ttg	1075
Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val Gly Leu Ala Ala Leu	

310	315	320	325	
atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat				1123
Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn				
330		335	340	
atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg				1171
Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu				
345		350	355	
gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc				1219
Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala				
360		365	370	
aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg				1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val				
375		380	385	
ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca				1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro				
390		395	400	405
cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt				1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe				
410		415	420	
ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac				1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp				
425		430	435	
aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga				1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly				
440		445	450	
ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg				1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr				
455		460	465	
gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg				1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val				
470		475	480	485
gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc				1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile				
490		495	500	
ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa				1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu				
505		510	515	
aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc				1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu				
520		525	530	
atg gca ttg gta ttt ggt tcg gtg att ttg ccg gcg aag gcc atc atc				1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile				
535		540	545	
atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg				1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met				
550		555	560	565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca 1843  
 Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro  
 570 575 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt 1891  
 Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu  
 585 590 595

tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc 1939  
 Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg  
 600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987  
 Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His  
 615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035  
 Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys  
 630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083  
 Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe  
 650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131  
 Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu  
 665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179  
 Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly  
 680 685 690

acc cgg ctt cgt taaaaaggcc tacacgtca tgg 2214  
 Thr Arg Leu Arg  
 695

&lt;210&gt; 362

&lt;211&gt; 697

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 362

Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val  
 1 5 10 15

Pro Leu Val Val Ile Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly  
 20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly  
 35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg  
 50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr  
 65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp  
 85 90 95



Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr  
 100 105 110  
 Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr  
 115 120 125  
 Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp  
 130 135 140  
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly  
 145 150 155 160  
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp  
 165 170 175  
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro  
 180 185 190  
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala  
 195 200 205  
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly  
 210 215 220  
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln  
 225 230 235 240  
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu  
 245 250 255  
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val  
 260 265 270  
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val  
 275 280 285  
 Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe  
 290 295 300  
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val  
 305 310 315 320  
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser  
 325 330 335  
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg  
 340 345 350  
 Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp  
 355 360 365  
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu  
 370 375 380  
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn  
 385 390 395 400  
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg  
 405 410 415

Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val  
 420 425 430  
 Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala  
 435 440 445  
 Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr  
 450 455 460  
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu  
 465 470 475 480  
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly  
 485 490 495  
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile  
 500 505 510  
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu  
 515 520 525  
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro  
 530 535 540  
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly  
 545 550 555 560  
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn  
 565 570 575  
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala  
 580 585 590  
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg  
 595 600 605  
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg  
 610 615 620  
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile  
 625 630 635 640  
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met  
 645 650 655  
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr  
 660 665 670  
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg  
 675 680 685  
 Arg Gln Leu Val Gly Thr Arg Leu Arg  
 690 695

&lt;210&gt; 363

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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 <222> (101)..(706)  
 <223> RXS03042

<400> 363

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tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc 115  
 Leu Val Leu Ala Phe  
 1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163  
 Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala  
 10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211  
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val  
 25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259  
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro  
 40 45 50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307  
 Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu  
 55 60 65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355  
 Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe  
 70 75 80 85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403  
 Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His  
 90 95 100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451  
 Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe  
 105 110 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499  
 Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe  
 120 125 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547  
 Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met  
 135 140 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595  
 Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu  
 150 155 160 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643  
 Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu  
 170 175 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691  
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn  
 185 190 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729  
 Val Gly Val Gly Ala

200

<210> 364  
 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 364  
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           1                  5                  10                  15  
 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr  
                   20                  25                  30  
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile  
           35                  40                  45  
 Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly  
           50                  55                  60  
 Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg  
           65                  70                  75                  80  
 Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser  
                   85                  90                  95  
 Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile  
           100                  105                  110  
 Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile  
           115                  120                  125  
 Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe  
           130                  135                  140  
 Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp  
           145                  150                  155                  160  
 Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val  
                   165                  170                  175  
 Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu  
           180                  185                  190  
 Glu Leu Lys Glu Asn Val Gly Val Gly Ala  
           195                  200

<210> 365  
 <211> 826  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(826)  
 <223> RXS03075

<400> 365  
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agcccagaag aacagtcaac tcctagatta aaggataatc	gtg gcg aaa ttc ctg	115
	Val Ala Lys Phe Leu	
	1 5	
tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg	163	
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala		
	10 15 20	
gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat	211	
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr		
	25 30 35	
gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc	259	
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val		
	40 45 50	
acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca	307	
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala		
	55 60 65	
aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag	355	
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys		
	70 75 80 85	
acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat	403	
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp		
	90 95 100	
gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat	451	
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp		
	105 110 115	
cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg	499	
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu		
	120 125 130	
gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg	547	
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser		
	135 140 145	
att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act	595	
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr		
	150 155 160 165	
ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag	643	
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys		
	170 175 180	
gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc	691	
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val		
	185 190 195	
tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc	739	
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr		
	200 205 210	
tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc	787	
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr		
	215 220 225	

ttc ggt tgc ttc atc gct gcc ggt atg ccg ctg atc tct  
 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser  
 230 235 240

826

<210> 366  
 <211> 242  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 366  
 Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys  
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 Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr  
 20 25 30  
 Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro  
 35 40 45  
 Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro  
 50 55 60  
 Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln  
 65 70 75 80  
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val  
 85 90 95  
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala  
 100 105 110  
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln  
 115 120 125  
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala  
 130 135 140  
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly  
 145 150 155 160  
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala  
 165 170 175  
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly  
 180 185 190  
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr  
 195 200 205  
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val  
 210 215 220  
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu  
 225 230 235 240  
 Ile Ser

<210> 367

<211> 983  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(960)  
 <223> RXS03124

<400> 367  
 atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac 48  
 Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp  
 1 5 10 15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag 96  
 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln  
 20 25 30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc 144  
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg  
 35 40 45

acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc 192  
 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly  
 50 55 60

act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct 240  
 Thr Ala Gly Ser Ala Val Phe Ala Gly Thr Thr Val Leu Ile Ala  
 65 70 75 80

ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc 288  
 Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala  
 85 90 95

att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc 336  
 Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser  
 100 105 110

ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca 384  
 Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala  
 115 120 125

cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg 432  
 Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr  
 130 135 140

atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac 480  
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr  
 145 150 155 160

ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc 528  
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr  
 165 170 175

aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc 576  
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr  
 180 185 190

gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc 624  
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly  
 195 200 205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag 672  
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu  
 210 215 220  
  
 gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac 720  
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn  
 225 230 235 240  
  
 act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc 768  
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe  
 245 250 255  
  
 gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc 816  
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser  
 260 265 270  
  
 gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg 864  
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser  
 275 280 285  
  
 ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt 912  
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe  
 290 295 300  
  
 acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc 960  
 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe  
 305 310 315 320  
  
 tgatcgtttt gggttagcg ttc 983

&lt;210&gt; 368

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 368

Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp  
1 5 10 15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln  
20 25 30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg  
35 40 45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly  
50 55 60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala  
65 70 75 80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala  
85 90 95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser  
100 105 110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala  
115 120 125



Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr  
 130 135 140  
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr  
 145 150 155 160  
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr  
 165 170 175  
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr  
 180 185 190  
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly  
 195 200 205  
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu  
 210 215 220  
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn  
 225 230 235 240  
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe  
 245 250 255  
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser  
 260 265 270  
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser  
 275 280 285  
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe  
 290 295 300  
 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe  
 305 310 315 320

&lt;210&gt; 369

&lt;211&gt; 271

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(271)

&lt;223&gt; RXS03125

&lt;400&gt; 369

tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60  
 tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115  
 Leu Val Leu Ala Phe  
 1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163  
 Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala  
 10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211  
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val

25 30 35  
 gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259  
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro  
 40 45 50  
 ctg ctg tgc ttc 271  
 Leu Leu Cys Phe  
 55  
 <210> 370  
 <211> 57  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 370  
 Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp  
 1 5 10 15  
 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr  
 20 25 30  
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile  
 35 40 45  
 Asp Asp Pro Gln Pro Leu Leu Cys Phe  
 50 55  
 <210> 371  
 <211> 576  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
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 <222> (101)..(553)  
 <223> RXA00596  
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 ccatcggagt gccaaagccct agctaccagg gaggaacta atg ctt aac gcc ctg 115  
 Met Leu Asn Ala Leu  
 1 5  
 aaa ttc atc cca tgg ctg atc ggc cag att ttc ctc tct ggc ttc agc 163  
 Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser  
 10 15 20  
 gtg atc acc gct gcg gta aaa aag gac acc ggc ttc aac ccc gtt gtt 211  
 Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val  
 25 30 35  
 atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg 259  
 Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu  
 40 45 50  
 tca acg tgc atc acc gcg act cct tcc acc ctg tcc ctt ggc cta cgc 307  
 Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg

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<400> 372
Met Leu Asn Ala Leu Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe
  1           5           10           15
Leu Ser Gly Phe Ser Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly
      20           25
Phe Asn Pro Val Val Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe
      35           40           45
Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu
      50           55           60
Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu
  65           70           75           80
Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser
      85           90           95
Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp
      100           105           110
His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp
      115           120           125
Ala Glu Trp Pro Ser Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val
      130           135           140
Ser Gln Asp Lys Arg Glu Phe

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150

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<220>  
<221> CDS  
<222> (101)..(715)  
<223> RXA02079
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<400> 373																						
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ctcccactac tgcccaaact gccagaagcg gcgctagctg																atg	agc	gaa	gct	ttt		115
																Met	Ser	Glu	Ala	Phe		
																1				5		
gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac																					163	
Asp	Ala	Thr	Lys	Val	Arg	Lys	Ala	Val	Leu	Thr	Val	Ala	Leu	Leu	Asn							
				10					15					20								
ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc																					211	
Phe	Ala	Tyr	Phe	Phe	Val	Glu	Phe	Phe	Ile	Ala	Leu	Ser	Ala	Gly	Ser							
				25					30					35								
gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc																					259	
Val	Ser	Leu	Leu	Ala	Asp	Ser	Val	Asp	Phe	Leu	Glu	Asp	Thr	Ser	Ile							
			40					45					50									
aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca																					307	
Asn	Leu	Leu	Ile	Phe	Ile	Ala	Leu	Gly	Trp	Pro	Leu	Ala	Arg	Arg	Ala							
			55					60					65									
gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt																					355	
Val	Met	Gly	Lys	Leu	Met	Ala	Ile	Val	Ile	Leu	Ala	Pro	Ala	Ala	Phe							
70					75					80					85							
gct gcg tgg gca gcg att caa ccg ttt tcc gca ccg caa gcg ccc gaa																					403	
Ala	Ala	Trp	Ala	Ala	Ile	Gln	Arg	Phe	Ser	Ala	Pro	Gln	Ala	Pro	Glu							
				90					95					100								
gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc																					451	
Val	Phe	Pro	Ile	Ile	Val	Ala	Ser	Leu	Gly	Ala	Val	Val	Ile	Asn	Gly							
			105					110					115									
gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt																					499	
Ala	Ser	Ala	Ile	Ile	Ile	Ser	Arg	Val	Arg	Gln	His	Gly	Gly	Ser	Leu							
			120					125					130									
ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att																					547	
Gly	Gln	Ala	Ala	Phe	Leu	Ser	Ala	Arg	Asn	Asp	Val	Leu	Ile	Asn	Ile							
			135					140					145									
gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg																					595	
Ala	Ile	Ile	Met	Met	Ala	Leu	Ile	Thr	Ala	Trp	Thr	Thr	Ser	Gly	Trp							
150					155					160					165							
cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc																					643	

Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala  
 170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691  
 Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys  
 185 190 195

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738  
 Ala Leu Ala Gly Glu Ala Ile Asp  
 200 205

<210> 374

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr  
 1 5 10 15

Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala  
 20 25 30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu  
 35 40 45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro  
 50 55 60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu  
 65 70 75 80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala  
 85 90 95

Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala  
 100 105 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln  
 115 120 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp  
 130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp  
 145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu  
 165 170 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu  
 180 185 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp  
 195 200 205

<210> 375

<211> 1458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1435)

<223> RXA01303

<400> 375

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aacatgcggg cgcaggtcag agctgttatc ttagtactta tcacagccat agggcggggt 60
tgacggaaaag cctttccgcg taaccatgaa gaggcacac  gtg aca caa ctc aac 115
                                         Val Thr Gln Leu Asn
                                         1                               5

acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
                               10                               15                               20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
                               25                               30                               35

atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc 259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro
                               40                               45                               50

cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg 307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp
                               55                               60                               65

ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac 355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr
                               70                               75                               80                               85

atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc 403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser
                               90                               95                               100

tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa 451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln
                               105                               110                               115

gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act 499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr
                               120                               125                               130

ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac 547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr
                               135                               140                               145

ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt 595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly
                               150                               155                               160                               165

atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc 643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val
                               170                               175                               180

atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc 691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr
                               185                               190                               195

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att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val 200 205 210	739
ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp 215 220 225	787
gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn 230 235 240 245	835
aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala 250 255 260	883
ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe 265 270 275	931
ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His 280 285 290	979
gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val 295 300 305	1027
cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp 310 315 320 325	1075
acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala 330 335 340	1123
atc ttc cta agc aga gcg gag aca cct gat gat ttc tgg cca ttc ctg Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp Phe Trp Pro Phe Leu 345 350 355	1171
tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly 360 365 370	1219
acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly 375 380 385	1267
gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val 390 395 400 405	1315
ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys 410 415 420	1363
gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala 425 430 435	1411

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga  
 Arg Pro Asn Ala Pro Phe Pro Gly  
           440                  445

1458

<210> 376  
 <211> 445  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 376  
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 Glu Asp Pro Glu His Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp  
           20                  25                  30  
 Ile Thr Thr Phe Ser Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val  
           35                  40                  45  
 Ser Ala Ile Ala Pro Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala  
   50                  55                  60  
 Gly Gln Leu Tyr Trp Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu  
   65                  70                  75                  80  
 Ile Arg Leu Ile Tyr Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys  
           85                  90                  95  
 Leu Val Gly Ile Ser Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp  
           100                  105                  110  
 Phe Leu Ala Val Gln Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr  
   115                  120                  125  
 Leu Ala Ala Leu Thr Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met  
   130                  135                  140  
 Pro Ser Thr Gly Tyr Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu  
   145                  150                  155                  160  
 Gly Ile Gln Ala Gly Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe  
           165                  170                  175  
 Met Gly Pro Trp Val Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu  
           180                  185                  190  
 Thr Pro Gln Arg Thr Ile Glu Gly Thr Thr Val Phe Val His Asn Ala  
           195                  200                  205  
 Ala Ile Val Leu Val Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe  
   210                  215                  220  
 Leu Phe Leu Lys Asp Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile  
   225                  230                  235                  240  
 Asp Ile Phe Gly Asn Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu  
           245                  250                  255  
 Met Thr Phe Gly Ala Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile  
           260                  265                  270



Ile Asn Asn Asn Phe Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro  
275 280 285

Ala Glu Met Leu His Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu  
290 295 300

Ile Gly Ala Leu Val Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe  
305 310 315 320

Gly Gly Ala Ile Trp Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala  
325 330 335

Thr Ala Ala Ala Ala Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp  
340 345 350

Phe Trp Pro Phe Leu Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly  
355 360 365

Leu Gly Asn Ala Gly Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys  
370 375 380

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe  
385 390 395 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala  
405 410 415

Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr  
420 425 430

Trp Ile Tyr Tyr Ala Arg Pro Asn Ala Pro Phe Pro Gly  
435 440 445

<210> 377

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA02079

<400> 377

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ctcccactac tgcccaaact gccagaagcg gcgctagctg atg agc gaa gct ttt 115  
Met Ser Glu Ala Phe  
1 5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163  
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn  
10 15 20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211  
Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser  
25 30 35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259

Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile  
40 45 50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca 307  
Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala  
55 60 65

gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt 355  
Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe  
70 75 80 85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa 403  
Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu  
90 95 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451  
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly  
105 110 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt 499  
Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu  
120 125 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547  
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile  
135 140 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg 595  
Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp  
150 155 160 165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc 643  
Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala  
170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691  
Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys  
185 190 195

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738  
Ala Leu Ala Gly Glu Ala Ile Asp  
200 205

&lt;210&gt; 378

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr  
1 5 10 15

Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala  
20 25 30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu  
35 40 45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro  
50 55 60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu  
 65 70 75 80  
 Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala  
 85 90 95  
 Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala  
 100 105 110  
 Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln  
 115 120 125  
 His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp  
 130 135 140  
 Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp  
 145 150 155 160  
 Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu  
 165 170 175  
 Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu  
 180 185 190  
 Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp  
 195 200 205

<210> 379  
 <211> 1173  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1150)  
 <223> RXN00832

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 ggaacggccc agagttctta agaaagtttg actagagaac atg ccg ttt tct tgg 115  
 Met Pro Phe Ser Trp  
 1 5  
 cta aaa cca att gat tat gcc cgc atc ttt gtc ggc tgg gca tcg att 163  
 Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val Gly Trp Ala Ser Ile  
 10 15 20  
 ttt atc atc ccc ctc atc aca ctg cca tca att att gag ttg gcg ctg 211  
 Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile Ile Glu Leu Ala Leu  
 25 30 35  
 atc gtg gca gtc atc cta ttc tgc gca ttt ggc gtg gtg aag atg gcg 259  
 Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly Val Val Lys Met Ala  
 40 45 50  
 gag cgt ttg gct cat att ttg ggt gat cct ttt gga tcg ttg atc ctt 307  
 Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe Gly Ser Leu Ile Leu  
 55 60 65

acc ttg tcg atc gtg atc att gaa gtg att ttg atc tgt gcg gtg atg Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu Ile Cys Ala Val Met 70 75 80 85	355
ctg ggg cct gct gat tca acc act gct ggt cgg gat tcc gtg atg gca Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg Asp Ser Val Met Ala 90 95 100	403
gtg tcc atg atc atc atg ggt ttg gtc gtg gga ttg tgc cta ctc att Val Ser Met Ile Ile Met Gly Leu Val Val Gly Leu Cys Leu Leu Ile 105 110 115	451
ggt ggt tta agg cat gga agc atg cca cac aat ggg gtg gga act ccg Gly Gly Leu Arg His Gly Ser Met Pro His Asn Gly Val Gly Thr Pro 120 125 130	499
acc tac ttg gtg ctg atc gca act ttt tcc gta atc gcc ttt gcg gtt Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val Ile Ala Phe Ala Val 135 140 145	547
cca gct ttc agg gga gaa tac tcc act ggg cag gca ctt gtt att tca Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln Ala Leu Val Ile Ser 150 155 160 165	595
aca ctg aca gca gtg gtg tac ggg ttc ttc ctg ttt cgc caa atg ggt Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly 170 175 180	643
gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp 185 190 195	691
gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile 200 205 210	739
act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met 215 220 225	787
gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu 230 235 240 245	835
att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys 250 255 260	883
gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly 265 270 275	931
gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile 280 285 290	979
ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn 295 300 305	1027

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc 1075  
 Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser  
 310 315 320 325

tcc aag aaa gtc agt gct gtg cat ggc tcg gtg ctg ctc atg ctt ttc 1123  
 Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe  
 330 335 340

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg 1170  
 Gly Val Tyr Met Met Ser Met Phe Ala  
 345 350

gaa 1173

<210> 380

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Pro Phe Ser Trp Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val  
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Gly Trp Ala Ser Ile Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile  
 20 25 30

Ile Glu Leu Ala Leu Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly  
 35 40 45

Val Val Lys Met Ala Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe  
 50 55 60

Gly Ser Leu Ile Leu Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu  
 65 70 75 80

Ile Cys Ala Val Met Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg  
 85 90 95

Asp Ser Val Met Ala Val Ser Met Ile Ile Met Gly Leu Val Val Gly  
 100 105 110

Leu Cys Leu Leu Ile Gly Gly Leu Arg His Gly Ser Met Pro His Asn  
 115 120 125

Gly Val Gly Thr Pro Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val  
 130 135 140

Ile Ala Phe Ala Val Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln  
 145 150 155 160

Ala Leu Val Ile Ser Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu  
 165 170 175

Phe Arg Gln Met Gly Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val  
 180 185 190

Ala Glu Lys Ala Asp Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly  
 195 200 205

Leu Ile Leu Ile Ile Thr Val Leu Pro Ile Val Leu Leu Ser His Asp

210	215	220
Met Ala Thr Val Met Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val		
225	230	235 240
Ala Met Ala Gly Leu Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr		
	245	250 255
Ile Thr Ser Leu Lys Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser		
	260	265 270
Asn Leu Ala His Gly Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro		
	275	280 285
Ala Val Leu Val Ile Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly		
	290	295 300
Glu Thr Pro Ile Asn Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr		
305	310	315 320
Ala Ile Ala Phe Ser Ser Lys Lys Val Ser Ala Val His Gly Ser Val		
	325	330 335
Leu Leu Met Leu Phe Gly Val Tyr Met Met Ser Met Phe Ala		
	340	345 350

<210> 381  
 <211> 578  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(555)  
 <223> FRXA00832

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Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly	
1 5 10 15	
gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac	96
Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp	
20 25 30	
gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc	144
Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile	
35 40 45	
act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg	192
Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met	
50 55 60	
gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta	240
Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu	
65 70 75 80	
att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa	288
Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys	
85 90 95	

gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga 336  
 Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly  
                   100                                  105                                  110

gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc 384  
 Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile  
                   115                                  120                                  125

ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac 432  
 Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn  
                   130                                  135                                  140

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc 480  
 Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser  
                   145                                  150                                  155                                  160

tcc aag aaa gtc agt gct gtg cat ggc tgc gtg ctg ctc atg ctt ttc 528  
 Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe  
                                   165                                  170                                  175

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg 575  
 Gly Val Tyr Met Met Ser Met Phe Ala  
                                   180                                  185

gaa 578

&lt;210&gt; 382

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 382

Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly  
   1                                  5                                  10                                  15

Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp  
                   20                                  25                                  30

Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile  
                   35                                  40                                  45

Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met  
                   50                                  55                                  60

Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu  
                   65                                  70                                  75                                  80

Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys  
                                   85                                  90                                  95

Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly  
                   100                                  105                                  110

Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile  
                   115                                  120                                  125

Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn  
                   130                                  135                                  140

Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser  
145 150 155 160

Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe  
165 170 175

Gly Val Tyr Met Met Ser Met Phe Ala  
180 185

<210> 383

<211> 2733

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2710)

<223> RXN00378

<400> 383

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cccaagaagg tttatcgtga gcacaccgga ttcttcctcg gtg gac aag gcc gta 115  
Val Asp Lys Ala Val  
1 5

aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163  
Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val  
10 15 20

gga ttg aac cga gcc acc gcc tca gaa gaa gag gaa gat tta agc tca 211  
Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser  
25 30 35

agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259  
Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala  
40 45 50

cca tcg ttg atg gtg gtg gaa aaa gcc cta gag aag atc ccc ggt gta 307  
Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val  
55 60 65

tcc gcg gat ctg att tac cct tca caa act gca tgg att aca gca act 355  
Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr  
70 75 80 85

gat cgg gta cat ccc gaa acc ctc att gag gtg ttt gag cag ttc ggc 403  
Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly  
90 95 100

atc aaa gca cac ctt tct aat tca tcg ctg ctg cgc agg cat caa cag 451  
Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln  
105 110 115

ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499  
Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser  
120 125 130

cga atg gat gcc aag cga atc tcg cct cgt gtg cga agg cat aac cga 547  
Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg



135	140	145	
caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa			595
Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys			
150	155	160	165
cgc agg aat cac acc acc tcg cag cat gaa gac cca atg tcg ggc gat			643
Arg Arg Asn His Thr Thr Ser Gln His Glu Asp Pro Met Ser Gly Asp			
	170	175	180
gtg ctg ttc acc gcc cgc gca ctg att aca cct aag cgt ttg tgg gtg			691
Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro Lys Arg Leu Trp Val			
	185	190	195
tcg ttg ccg ttt gcg ctc atc gta ttg gcg tta tcg ttg aat cct tcg			739
Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu Ser Leu Asn Pro Ser			
	200	205	210
tgg cag ttt gat tat tgg cag tgg ttg tcc gct gtg ttg gct att cct			787
Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala Val Leu Ala Ile Pro			
	215	220	225
gtg gtg gtg tgg ggt gcc tgg ccg ttt cac cgc gct gca gca ggc ggt			835
Val Val Val Trp Gly Ala Trp Pro Phe His Arg Ala Ala Ala Gly Gly			
	230	235	240
att cgt cga gga att tcc gct ctt gat gcg acc agc tca atc gct att			883
Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr Ser Ser Ile Ala Ile			
	250	255	260
gct gct gca tac gcg tgg tct atc gcc atg ctg ttg ttt gaa acc cca			931
Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu Leu Phe Glu Thr Pro			
	265	270	275
gga ggt aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac			979
Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His			
	280	285	290
ggc acg ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc			1027
Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile			
	295	300	305
acc gtg ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa			1075
Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln			
	310	315	320
tcc agt ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc			1123
Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg			
	330	335	340
att gtc act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa			1171
Ile Val Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu			
	345	350	355
ctg aac att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt			1219
Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val			
	360	365	370
cca cct aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt			1267
Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly			
	375	380	385

tcg cgg atc gca gct agc atc atc atg gga caa gac cag cgt gat gta	1315
Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val	
390 395 400 405	
aaa gta aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa	1363
Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu	
410 415 420	
atc aag gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg	1411
Ile Lys Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala	
425 430 435	
gta cat agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat	1459
Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn	
440 445 450	
agg gca gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc	1507
Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr	
455 460 465	
ctt gct gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc	1555
Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile	
470 475 480 485	
aac gct gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg	1603
Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro	
490 495 500	
gtg gcc tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa	1651
Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu	
505 510 515	
gct gca gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga	1699
Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg	
520 525 530	
gtt ctc gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta	1747
Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu	
535 540 545	
acc gat ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag	1795
Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu	
550 555 560 565	
gac cca gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc	1843
Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser	
570 575 580	
cac cac gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt	1891
His His Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg	
585 590 595	
gat acc ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc	1939
Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly	
600 605 610	
aac gtg gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg	1987
Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu	
615 620 625	

cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala 630 635 640 645	2035
ctc ctg tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser 650 655 660	2083
ccc cga cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val 665 670 675	2131
cga tgg aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val 680 685 690	2179
aga tca gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile 695 700 705	2227
gag acc atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr 710 715 720 725	2275
gca gac agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly 730 735 740	2323
aag aaa gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc Lys Lys Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val 745 750 755	2371
gcg atg atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp 760 765 770	2419
gtg ggt gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat Val Gly Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp 775 780 785	2467
tcc gat gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg Ser Asp Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met 790 795 800 805	2515
agc gtg ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val 810 815 820	2563
aat ggc aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val 825 830 835	2611
ctt gca gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg Leu Ala Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met 840 845 850	2659
ctg gcg tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys 855 860 865	2707
tac taaccagcaa ttcccaagcc caa	2733

Tyr  
870

<210> 384  
<211> 870  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 384  
Val Asp Lys Ala Val Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala  
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Leu Lys Ala Gly Val Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu  
20 25 30  
Glu Asp Leu Ser Ser Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu  
35 40 45  
Gly Leu Ser Asn Ala Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu  
50 55 60  
Lys Ile Pro Gly Val Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala  
65 70 75 80  
Trp Ile Thr Ala Thr Asp Arg Val His Pro Glu Thr Leu Ile Glu Val  
85 90 95  
Phe Glu Gln Phe Gly Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu  
100 105 110  
Arg Arg His Gln Gln Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu  
115 120 125  
Asp Arg Tyr Arg Ser Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val  
130 135 140  
Arg Arg His Asn Arg Gln Glu Met Val His Ala Val Arg Ala Arg Glu  
145 150 155 160  
Ser Gly Trp Ile Lys Arg Arg Asn His Thr Thr Ser Gln His Glu Asp  
165 170 175  
Pro Met Ser Gly Asp Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro  
180 185 190  
Lys Arg Leu Trp Val Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu  
195 200 205  
Ser Leu Asn Pro Ser Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala  
210 215 220  
Val Leu Ala Ile Pro Val Val Val Trp Gly Ala Trp Pro Phe His Arg  
225 230 235 240  
Ala Ala Ala Gly Gly Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr  
245 250 255  
Ser Ser Ile Ala Ile Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu  
260 265 270

Leu Phe Glu Thr Pro Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp  
 275 280 285  
 Phe Ala Phe Asp His Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp  
 290 295 300  
 Val Ala Cys Gly Ile Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr  
 305 310 315 320  
 Arg Arg Arg Ser Gln Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln  
 325 330 335  
 Ile Asp Pro Gln Arg Ile Val Thr Val Val Arg Lys His Arg Leu Lys  
 340 345 350  
 Arg Val Val Gln Glu Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn  
 355 360 365  
 Asp Asp Val Lys Val Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr  
 370 375 380  
 Val Ile Gly Gly Gly Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln  
 385 390 395 400  
 Asp Gln Arg Asp Val Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu  
 405 410 415  
 Asn Leu Glu Ser Glu Ile Lys Val Arg Val Ile Arg Thr Gly His Arg  
 420 425 430  
 Thr Arg Ile Ala Ala Val His Arg Trp Val Lys Glu Ala Thr Leu Lys  
 435 440 445  
 Glu Asn Arg His Asn Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val  
 450 455 460  
 Pro Ile Thr Phe Thr Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu  
 465 470 475 480  
 Ile Ser Gly Asn Ile Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu  
 485 490 495  
 Ala Cys Val Ala Pro Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr  
 500 505 510  
 Arg Asn Ser Ile Glu Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser  
 515 520 525  
 Gly Glu Ile Phe Arg Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn  
 530 535 540  
 Arg Val Gly Thr Leu Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr  
 545 550 555 560  
 Ala Asp Lys Gly Glu Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala  
 565 570 575  
 Leu Ala Met Glu Ser His His Ala Ile Ser Lys Ala Leu Val Lys Ala  
 580 585 590  
 Ser Arg Glu Ala Arg Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His

595	600	605
Trp Ile Glu Val Gly Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln 610 615 620		
Ala Thr Ile Glu Leu Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met 625 630 635 640		
Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val 645 650 655		
Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly 660 665 670		
Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr 675 680 685		
Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile 690 695 700		
Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro 705 710 715 720		
Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala 725 730 735		
Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr 740 745 750		
Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys 755 760 765		
Leu Lys Val Ala Asp Val Gly Val Leu Met Gly Val Asp Arg Pro Ser 770 775 780		
Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met 785 790 795 800		
Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg 805 810 815		
Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn 820 825 830		
Gly Val Ala Met Val Leu Ala Val Ser Gly Leu Leu His Pro Met Ala 835 840 845		
Ala Thr Val Ala Met Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser 850 855 860		
Gly Arg Ala Arg Lys Tyr 865 870		

&lt;210&gt; 385

&lt;211&gt; 1796

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1773)

&lt;223&gt; FRXA00378

&lt;400&gt; 385

aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac ggc acg	48
Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr	
1 5 10 15	
ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc acc gtg	96
Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val	
20 25 30	
ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa tcc agt	144
Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser	
35 40 45	
ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc att gtc	192
Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val	
50 55 60	
act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa ctg aac	240
Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn	
65 70 75 80	
att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt cca cct	288
Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro	
85 90 95	
aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt tcg cgg	336
Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg	
100 105 110	
atc gca gct agc atc atc atg gga caa gac cag cgt gat gta aaa gta	384
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val	
115 120 125	
aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa atc aag	432
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys	
130 135 140	
gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg gta cat	480
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His	
145 150 155 160	
agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat agg gca	528
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala	
165 170 175	
gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc ctt gct	576
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala	
180 185 190	
gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc aac gct	624
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala	
195 200 205	
gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg gtg gcc	672
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala	
210 215 220	
tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa gct gca	720

Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala	
225 230 235 240	
gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga gtt ctc	768
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu	
245 250 255	
gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta acc gat	816
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp	
260 265 270	
ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag gac cca	864
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro	
275 280 285	
gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc cac cac	912
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His	
290 295 300	
gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt gat acc	960
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr	
305 310 315 320	
ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc aac gtg	1008
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val	
325 330 335	
gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg cca ctg	1056
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu	
340 345 350	
atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca ctc ctg	1104
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu	
355 360 365	
tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc ccc cga	1152
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg	
370 375 380	
cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg cga tgg	1200
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp	
385 390 395 400	
aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg aga tca	1248
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser	
405 410 415	
gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc gag acc	1296
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr	
420 425 430	
atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac gca gac	1344
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp	
435 440 445	
agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc aag aaa	1392
Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys	
450 455 460	
gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc gcg atg	1440
Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met	



465	470	475	480	
atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac gtg ggt				1488
Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly	485	490	495	
gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat tcc gat				1536
Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp	500	505	510	
gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg agc gtg				1584
Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val	515	520	525	
ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc aat ggc				1632
Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly	530	535	540	
aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg ctt gca				1680
Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala	545	550	555	560
gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg ctg gcg				1728
Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala	565	570	575	
tct tcg ctg ctt att gaa tgg cgc tcg gcc agg gcg cgc aag tac				1773
Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr	580	585	590	
taaccagcaa ttcccaagcc caa				1796
<p>&lt;210&gt; 386</p> <p>&lt;211&gt; 591</p> <p>&lt;212&gt; PRT</p> <p>&lt;213&gt; Corynebacterium glutamicum</p>				
<p>&lt;400&gt; 386</p> <p>Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr</p> <p>1 5 10 15</p> <p>Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val</p> <p>20 25 30</p> <p>Ile Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser</p> <p>35 40 45</p> <p>Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val</p> <p>50 55 60</p> <p>Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn</p> <p>65 70 75 80</p> <p>Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro</p> <p>85 90 95</p> <p>Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg</p> <p>100 105 110</p> <p>Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val</p>				

115	120	125
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys		
130	135	140
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His		
145	150	155
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala		
165	170	175
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala		
180	185	190
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala		
195	200	205
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala		
210	215	220
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala		
225	230	235
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu		
245	250	255
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp		
260	265	270
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro		
275	280	285
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His		
290	295	300
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr		
305	310	315
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val		
325	330	335
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu		
340	345	350
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu		
355	360	365
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg		
370	375	380
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp		
385	390	395
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser		
405	410	415
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr		
420	425	430
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp		
435	440	445

Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys  
450 455 460

Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met  
465 470 475 480

Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly  
485 490 495

Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp  
500 505 510

Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val  
515 520 525

Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly  
530 535 540

Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala  
545 550 555 560

Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala  
565 570 575

Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr  
580 585 590

<210> 387

<211> 327

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(304)

<223> RXA00942

<400> 387

cattgaccgg cagctcgtct gattcactgc acatcgtaca ttggacgggtg gacacgtttc 60

agagtccgct ggatttcattc acatcgggaag gaagagaatt ttg agt acc aaa aat 115  
Leu Ser Thr Lys Asn  
1 5

tac cac gtc gag ggt ttg acc tgc gca aac ggt gta gct tcc gta gag 163  
Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly Val Ala Ser Val Glu  
10 15 20

gat gaa atc ggc att gtt gcg ggc acc cag ggt gtg gat att gat att 211  
Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly Val Asp Ile Asp Ile  
25 30 35

gag acc ggc cgc gtc acg gtg act ggt gaa ggt ttc act gac gag gaa 259  
Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly Phe Thr Asp Glu Glu  
40 45 50

atc att gag gct gtc gcg aac gcg ggc tac aaa gtt tct ggg cgg 304  
Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys Val Ser Gly Arg  
55 60 65

tagcacaatt acacattcat etc

327

&lt;210&gt; 388

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 388

Leu Ser Thr Lys Asn Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly  
 1 5 10 15

Val Ala Ser Val Glu Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly  
 20 25 30

Val Asp Ile Asp Ile Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly  
 35 40 45

Phe Thr Asp Glu Glu Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys  
 50 55 60

Val Ser Gly Arg  
 65

&lt;210&gt; 389

&lt;211&gt; 1925

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1902)

&lt;223&gt; RXN01338

&lt;400&gt; 389

aaa act tat acc cca aat ccc tgg atg tta ttc atc cgc tca ttt gat 48  
 Lys Thr Tyr Thr Pro Asn Pro Trp Met Leu Phe Ile Arg Ser Phe Asp  
 1 5 10 15

ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata cat ctc att 96  
 Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile  
 20 25 30

tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac tgg cct tta 144  
 Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu  
 35 40 45

ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg gat gtg ctg 192  
 Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu  
 50 55 60

aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta gca gca gtc 240  
 Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val  
 65 70 75 80

tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt gcc gcg atc 288  
 Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile  
 85 90 95

atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag gca gca tca Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser 100 105 110	336
cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc gca cca agt Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser 115 120 125	384
aca gct cac cgc ctg ttg ggt gca acc att ctt gat gga acc gaa gag Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu 130 135 140	432
atc gcc gtg gaa gag atc acg gtt ggt gat tta gtg gcg gtg ctc ccg Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro 145 150 155 160	480
cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc cac ggc acc His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr 165 170 175	528
atg gat gag tct tat ctc acg ggt gag ccc tat gtg gtg agt aaa tct Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser 180 185 190	576
aaa ggt tcg caa gca atg tcg ggt gca gtc aat ggt gat act ccg ctg Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu 195 200 205	624
acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac gcc caa att Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile 210 215 220	672
gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa atg cgc agg Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg 225 230 235 240	720
atg gct gac cgt ctt ggc gcg tgg tat acg gtg att gca ctt gcc ctc Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu 245 250 255	768
ggt ggt ctt ggc tgg att gtc tcc ggc gac cca gtg agg ttc ttg gct Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala 260 265 270	816
gtt gtc gtt gtc gcc acc cca tgt cca ttg ctc att gca gtg cca gtg Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val 275 280 285	864
gcg atc atc ggt gcg att tct ctt gcg gct cgt cgg ggc atc atc gtg Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val 290 295 300	912
aag aac cct gga atg ctg gaa aac gct tca gga gta aag aca gtg atg Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met 305 310 315 320	960
ttc gat aag act gga acg ctc acc tat ggc agg cca gtg att act gat Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp 325 330 335	1008
atc cac act gct ccc gga gtt gag gaa gat aca gtc cta gct ttg gct	1056

Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala	340	345	350	
gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac gcg att cgt				1104
Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg	355	360	365	
gag ggc gca aaa gcc agg gaa ctt cat ctg cct gat gta gtg gaa gta				1152
Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val	370	375	380	
tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc gag cac ctg				1200
Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu	385	390	395	400
gtt cga ata acc aat agg cgc agc aca cta gaa att gat cca gac agc				1248
Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser	405	410	415	
aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct gtg gtg ctt				1296
Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu	420	425	430	
gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat gaa cct cgt				1344
Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg	435	440	445	
gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag cac aaa gtg				1392
Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val	450	455	460	
gac aag ctc atg att atc tct ggt gat cgc gca tct gag gtt cgt tac				1440
Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr	465	470	475	480
ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg				1488
Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro	485	490	495	
gaa gac aag ctg aac att gtt aat cgg cat aat gag cac ggc gcc acc				1536
Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr	500	505	510	
atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc				1584
Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala	515	520	525	
acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca				1632
Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala	530	535	540	
gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg				1680
Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu	545	550	555	560
ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa tct gcg ggc				1728
Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly	565	570	575	
ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg gta ttt gga				1776
Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly				

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<210> 390
<211> 634
<212> PRT
<213> Corynebacterium glutamicum
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Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile  
20 25 30

Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu  
35 40 45

Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu  
50 55 60

Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val  
65 70 75 80

Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile  
85 90 95

Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser  
100 105 110

Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser  
115 120 125

Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu  
130 135 140

Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro  
145 150 155 160

His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr  
165 170 175

Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser  
180 185 190

Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu  
195 200 205

Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile  
 210 215 220  
 Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg  
 225 230 235 240  
 Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu  
 245 250 255  
 Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala  
 260 265 270  
 Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val  
 275 280 285  
 Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val  
 290 295 300  
 Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met  
 305 310 315 320  
 Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp  
 325 330 335  
 Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala  
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 Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg  
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 Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val  
 370 375 380  
 Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu  
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 Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu  
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 Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val  
 450 455 460  
 Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr  
 465 470 475 480  
 Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro  
 485 490 495  
 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr  
 500 505 510  
 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala  
 515 520 525



Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala  
530 535 540

Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu  
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Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly  
565 570 575

Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly  
580 585 590

Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val  
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<211> 2001

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1978)

<223> FRXA01338

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Met Leu Phe Ile Arg  
1 5

tca ttt gat ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata 163  
Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile  
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cat ctc att tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac 211  
His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn  
25 30 35

tgg cct tta ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg 259  
Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp  
40 45 50

gat gtg ctg aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta 307  
Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu  
55 60 65

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Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val  
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gcc gcg atc atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag 403  
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90	95	100	
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gca cca agt aca gct cac cgc ctg ttg ggt gca acc att ctt gat gga Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly 120 125 130			499
acc gaa gag atc gcc gtg gaa gag atc acg gtt ggt gat tta gtg gcg Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala 135 140 145			547
gtg ctc ccg cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc Val Leu Pro His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly 150 155 160 165			595
cac ggc acc atg gat gag tct tat ctc acg ggt gag ccc tat gtg gtg His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val 170 175 180			643
agt aaa tct aaa ggt tcg caa gca atg tcg ggt gca gtc aat ggt gat Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp 185 190 195			691
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gcc caa att gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa Ala Gln Ile Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu 215 220 225			787
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ttc ttg gct gtt gtc gtt gtc gcc acc cca tgt cca ttg ctc att gca Phe Leu Ala Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala 265 270 275			931
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atc atc gtg aag aac cct gga atg ctg gaa aac gct tca gga gta aag Ile Ile Val Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys 295 300 305			1027
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gag cac ctg gtt cga ata acc aat agg cgc agc aca cta gaa att gat Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp 390 395 400 405	1315
cca gac agc aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser 410 415 420	1363
gtg gtg ctt gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp 425 430 435	1411
gaa cct cgt gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys 440 445 450	1459
cac aaa gtg gac aag ctc atg att atc tct ggt gat cgc gca tct gag His Lys Val Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu 455 460 465	1507
gtt cgt tac ctt gcg gac aag gtt ggc att gat gag gta cac gca gag Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu 470 475 480 485	1555
gcc tca ccg gaa gac aag ctg aac att gtt aat cgg cat aat gag cac Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His 490 495 500	1603
ggc gcc acc atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met 505 510 515	1651
gcc gtt gcc acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg Ala Val Ala Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr 520 525 530	1699
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gac gat ctg ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln 550 555 560 565	1795
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          20             25             30
Gly Leu Ala Lys Asn Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly
          35             40             45
Ile Pro Leu Met Trp Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly
          50             55             60
Gly Ala Asp Thr Leu Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu
          65             70             75             80
Gly Glu Trp Leu Val Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly
          85             90             95
Glu Ala Leu Glu Glu Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp
          100             105             110
Ala Leu Ala Arg Arg Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala
          115             120             125
Thr Ile Leu Asp Gly Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val
          130             135             140
Gly Asp Leu Val Ala Val Leu Pro His Glu Leu Cys Pro Val Asp Gly
          145             150             155             160
Glu Ile Val Ala Gly His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly
          165             170             175
Glu Pro Tyr Val Val Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly
          180             185             190
Ala Val Asn Gly Asp Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala
          195             200             205
His Asp Ser Arg Tyr Ala Gln Ile Val Gly Val Leu His Glu Ala Glu

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210	215	220
Asn Asn Arg Pro Glu Met Arg Arg Met Ala Asp Arg Leu Gly Ala Trp 225 230 235 240		
Tyr Thr Val Ile Ala Leu Ala Leu Gly Gly Leu Gly Trp Ile Val Ser 245 250 255		
Gly Asp Pro Val Arg Phe Leu Ala Val Val Val Val Ala Thr Pro Cys 260 265 270		
Pro Leu Leu Ile Ala Val Pro Val Ala Ile Ile Gly Ala Ile Ser Leu 275 280 285		
Ala Ala Arg Arg Gly Ile Ile Val Lys Asn Pro Gly Met Leu Glu Asn 290 295 300		
Ala Ser Gly Val Lys Thr Val Met Phe Asp Lys Thr Gly Thr Leu Thr 305 310 315 320		
Tyr Gly Arg Pro Val Ile Thr Asp Ile His Thr Ala Pro Gly Val Glu 325 330 335		
Glu Asp Thr Val Leu Ala Leu Ala Ala Ser Val Glu Arg Tyr Ser Arg 340 345 350		
His Pro Leu Ala Asp Ala Ile Arg Glu Gly Ala Lys Ala Arg Glu Leu 355 360 365		
His Leu Pro Asp Val Val Glu Val Ser Glu Arg Pro Gly Gln Gly Leu 370 375 380		
Thr Gly Thr Val Gly Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser 385 390 395 400		
Thr Leu Glu Ile Asp Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser 405 410 415		
Ser Gly Met Glu Ser Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu 420 425 430		
Ile Arg Leu Arg Asp Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala 435 440 445		
His Leu Pro Lys Lys His Lys Val Asp Lys Leu Met Ile Ile Ser Gly 450 455 460		
Asp Arg Ala Ser Glu Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp 465 470 475 480		
Glu Val His Ala Glu Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn 485 490 495		
Arg His Asn Glu His Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn 500 505 510		
Asp Ala Pro Ala Met Ala Val Ala Thr Val Gly Val Ala Met Gly Ala 515 520 525		
Asp Ser Asp Val Thr Ser Glu Ala Ala Asp Ala Val Ile Leu Asp Ser 530 535 540		

Ser Leu Glu Arg Leu Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg  
545 550 555 560

Arg Ile Ala Leu Gln Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile  
565 570 575

Gly Met Ile Leu Ala Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala  
580 585 590

Ile Phe Gln Glu Val Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg  
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Val Ala Leu Pro Arg Gly Ala Ile Ser Asp Phe Asp Thr Gln Glu Lys  
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Val Ser  
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(301)

<223> RXA01625

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Met Ala Ile Lys Asn  
1 5

tac acc gtc gaa ggc atg act tgt gga cac tgc gtc tcc tcc gta aag 163  
Tyr Thr Val Glu Gly Met Thr Cys Gly His Cys Val Ser Ser Val Lys  
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gaa gag gtc gga gag gtt gct ggc gtc acc gct gtg gac gtc acc cta 211  
Glu Glu Val Gly Glu Val Ala Gly Val Thr Ala Val Asp Val Thr Leu  
25 30 35

gaa acc ggt gcc gtg cag gtt acc ggc gaa gac ttc acc gac gag gct 259  
Glu Thr Gly Ala Val Gln Val Thr Gly Glu Asp Phe Thr Asp Glu Ala  
40 45 50

gtc aag gct gct gtc gtt gag gct ggc tac aag gtt gtt gca 301  
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taaaccctg aaaagtttaa agc 324

<210> 394

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Phe Thr Asp Glu Ala Val Lys Ala Ala Val Val Glu Ala Gly Tyr Lys  
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Val Val Ala  
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&lt;210&gt; 395

&lt;211&gt; 2799

&lt;212&gt; DNA

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&lt;223&gt; RXA02220

&lt;400&gt; 395

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 Val Ser Ser Pro Leu  
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ccc gct gcc gtc aca tca aaa ccc gcc cac gcg ctt tcc tct gat gag 163  
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 10 15 20

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gca aca cag cgt ttg gaa gca aac ggg cca aac gag ctt cct caa act 259  
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cca cct gaa aca gtc tgg caa cgg cta ttc cgc cag gtc aac gat cca 307  
 Pro Pro Glu Thr Val Trp Gln Arg Leu Phe Arg Gln Val Asn Asp Pro  
 55 60 65

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 Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu Thr Ala Phe Leu Gly  
 70 75 80 85

cat tgg aca gac acc atc gtg atc ggc gcc gtt gtc atc atc aac atg 403  
 His Trp Thr Asp Thr Ile Val Ile Gly Ala Val Val Ile Ile Asn Met  
 90 95 100

atg gtt ggg ttc atc caa gag ggc aaa gct gcg gat gcg ttg gca tgc 451  
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 105 110 115

atc cgc aac atg ctc tcc ccg gaa tcc gcg gcg ttg cgc gat ggg gtc Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala Leu Arg Asp Gly Val 120 125 130	499
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Val Ala Met Gly Ile Lys Gly Thr Glu Ala Thr Lys Asp Ala Ala Asp	
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Ile Val Leu Ala Asp Asp Asn Phe Ala Thr Ile Ala Gly Ala Val Glu	
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Leu Pro Thr Asn Gly Ala Gln Gly Leu Val Ile Phe Ile Ala Met Leu	
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710 715 720 725	
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Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr Val Leu Leu Leu	
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Asp Ile Asp Thr Ala Arg Thr Ile Ala Val Thr Thr Leu Ala Val Ser	
790 795 800 805	
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Gln Val Phe Tyr Leu Leu Ser Ser Arg Tyr Phe Glu Val Ser Ala Leu	
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cga aaa gaa ctc ttc acc acc aac ccg att tcc tgg ctg tgc atc gca	2611
Arg Lys Glu Leu Phe Thr Thr Asn Pro Ile Ser Trp Leu Cys Ile Ala	
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ctc atg ctg atc ctg caa ctg gcc ttt gtc tac ctg ccg ttc atg caa	2659
Leu Met Leu Ile Leu Gln Leu Ala Phe Val Tyr Leu Pro Phe Met Gln	

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Leu Val Phe Gly Val Val Phe Ala Val Val Glu Thr Glu Lys Phe			
870	875	880	885
atc agg cgc ctt aaa gcg tct taagggtttca gccctcaag ata			2799
Ile Arg Arg Leu Lys Ala Ser			
890			

<210> 396  
 <211> 892  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 396  
 Val Ser Ser Pro Leu Pro Ala Ala Val Thr Ser Lys Pro Ala His Ala  
 1 5 10 15  
 Leu Ser Ser Asp Glu Val Leu Glu Asn Leu Gly Val Gln Asp Thr Gly  
 20 25 30  
 Leu Thr Ser Ala Glu Ala Thr Gln Arg Leu Glu Ala Asn Gly Pro Asn  
 35 40 45  
 Glu Leu Pro Gln Thr Pro Pro Glu Thr Val Trp Gln Arg Leu Phe Arg  
 50 55 60  
 Gln Val Asn Asp Pro Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu  
 65 70 75 80  
 Thr Ala Phe Leu Gly His Trp Thr Asp Thr Ile Val Ile Gly Ala Val  
 85 90 95  
 Val Ile Ile Asn Met Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala  
 100 105 110  
 Asp Ala Leu Ala Ser Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala  
 115 120 125  
 Leu Arg Asp Gly Val Phe His Lys Ile Asp Ala Ala Glu Leu Val Val  
 130 135 140  
 Gly Asp Val Val Lys Leu Ser Ala Gly Asp Lys Val Pro Ala Asp Leu  
 145 150 155 160  
 Arg Met Leu Ala Ala Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr  
 165 170 175  
 Gly Glu Ala Glu Ala Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp  
 180 185 190  
 Ala Gly Ile Gly Asp Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val  
 195 200 205  
 Leu Thr Gly Ser Gly Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr

210	215	220
Glu Ile Gly His Ile Thr Thr Met Leu Ala Asp Val Asp Ser Val Asp 225	230	235 240
Thr Pro Leu Thr Arg Ser Met Lys Lys Phe Ser Ser Ala Leu Ala Ile 245	250	255
Val Cys Val Phe Leu Ala Ile Leu Met Leu Val Val Ala Gly Leu Val 260	265	270
His His Thr Pro Leu Glu Glu Leu Ile Leu Ser Ala Ile Gly Phe Ala 275	280	285
Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Ala Ile Thr Leu 290	295	300
Ala Leu Gly Val Gln Lys Met Ala Ala Arg Asn Ala Ile Thr Arg Arg 305	310	315 320
Leu Asn Ser Val Glu Thr Leu Gly Ser Val Thr Thr Ile Cys Thr Asp 325	330	335
Lys Thr Gly Thr Leu Thr Arg Asn Glu Met Thr Val Arg Ala Ile Ala 340	345	350
Thr Gly Thr Ser Leu Tyr Asp Val Ser Gly Ala Gly Tyr Glu Pro Leu 355	360	365
Gly Glu Ile Arg Leu Lys Asp Gly Glu Gln Val Ser Lys Gln Asp Phe 370	375	380
Pro Asp Leu Tyr Ala Met Ala Leu Val Ala Ala Asn Val Asn Asp Ala 385	390	395 400
Glu Ile Tyr Gln Glu Asp Gly Met Trp Arg Leu Ser Gly Glu Pro Thr 405	410	415
Asp Gly Gly Ile Arg Ala Phe Ala Met Lys Thr Asn Ala Glu Ile Leu 420	425	430
Thr Arg Thr Ala Glu Val Pro Phe Asp Ser Ala Tyr Lys Tyr Met Ala 435	440	445
Thr Leu His Thr Ile Asp Gly Ala Asn Thr Met Leu Val Lys Gly Ala 450	455	460
Pro Asp Arg Leu Leu Asp Arg Ser Ala Gln Gln Arg Asn Gly Glu Pro 465	470	475 480
Leu Asp Arg Pro Tyr Trp Glu Gln Leu Ile Glu Asp Leu Ala Ser Gln 485	490	495
Gly Leu Arg Val Leu Ala Ala Ala Tyr Lys Glu Leu Pro His Ser Thr 500	505	510
Ser Thr Ile Thr Pro Glu Asp Val Asp Gln Gly Glu Leu Thr Phe Leu 515	520	525
Gly Leu Tyr Gly Ile Met Asp Pro Pro Arg Glu Glu Val Ile Glu Ala 530	535	540

Met Lys Val Val Gln Ser Ala Gly Val Arg Val Arg Met Ile Thr Gly  
 545 550 555 560  
 Asp His Ser Ser Thr Ala Arg Ala Ile Ala Arg Glu Val Gly Ile Arg  
 565 570 575  
 Gly Gln Asn Val Leu Thr Gly Ala Glu Ile Thr Ala Ala Thr Asp Glu  
 580 585 590  
 Glu Leu Gln Gly Leu Val Asp Asn Ala Asp Leu Phe Val Arg Thr Ser  
 595 600 605  
 Pro Glu His Lys Leu Arg Val Val Arg Ala Leu Gln Ala Asn Gly Glu  
 610 615 620  
 Val Ala Ser Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Lys  
 625 630 635 640  
 Gln Ala Asp Val Gly Val Ala Met Gly Ile Lys Gly Thr Glu Ala Thr  
 645 650 655  
 Lys Asp Ala Ala Asp Ile Val Leu Ala Asp Asp Asn Phe Ala Thr Ile  
 660 665 670  
 Ala Gly Ala Val Glu Met Gly Arg Thr Ile Tyr Asp Asn Leu Arg Lys  
 675 680 685  
 Ala Val Val Phe Met Leu Pro Thr Asn Gly Ala Gln Gly Leu Val Ile  
 690 695 700  
 Phe Ile Ala Met Leu Leu Gly Trp Glu Leu Pro Ile Thr Ala Leu Gln  
 705 710 715 720  
 Val Leu Trp Ile Asn Leu Ile Thr Ala Ile Thr Leu Ser Leu Ala Leu  
 725 730 735  
 Ser Phe Glu Pro Ala Glu Pro Gly Ile Met Asn Arg Lys Pro Arg Asn  
 740 745 750  
 Pro Lys Ser Gly Leu Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr  
 755 760 765  
 Val Ser Leu Leu Leu Gly Gly Ala Thr Phe Trp Ala Phe Leu Gly Ala  
 770 775 780  
 Arg Asp Ala Gly Ile Asp Ile Asp Thr Ala Arg Thr Ile Ala Val Thr  
 785 790 795 800  
 Thr Leu Ala Val Ser Gln Val Phe Tyr Leu Leu Ser Ser Arg Tyr Phe  
 805 810 815  
 Glu Val Ser Ala Leu Arg Lys Glu Leu Phe Thr Thr Asn Pro Ile Ser  
 820 825 830  
 Trp Leu Cys Ile Ala Leu Met Leu Ile Leu Gln Leu Ala Phe Val Tyr  
 835 840 845  
 Leu Pro Phe Met Gln Ser Thr Phe Asp Thr Ala Ala Leu Thr Leu Arg  
 850 855 860

Asp Trp Val Met Pro Leu Val Phe Gly Val Val Val Phe Ala Val Val  
865 870 875 880

Glu Thr Glu Lys Phe Ile Arg Arg Leu Lys Ala Ser  
885 890

<210> 397  
<211> 1917  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1894)  
<223> RXN00980

<400> 397  
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cctcttgatt attttgtcgt ggttgagttc atcgagcccg atg ctg gca gat gca 115  
Met Leu Ala Asp Ala  
1 5  
ttc atg atc gcg gct gca att gtt gca ggt tgg ccg atc gcg cag tct 163  
Phe Met Ile Ala Ala Ile Val Ala Gly Trp Pro Ile Ala Gln Ser  
10 15 20  
gca tat caa gca ctt cgc att cga atg gtg tcg att gac tta ctg gtc 211  
Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser Ile Asp Leu Leu Val  
25 30 35  
gtt gtg gct gcc gtt ggt gcc atg ttc atc aac aac tat tgg gag tct 259  
Val Val Ala Ala Val Gly Ala Met Phe Ile Asn Asn Tyr Trp Glu Ser  
40 45 50  
gcg gcg gtg acg ttc ctc ttt gcc ctt ggc aag gca ctg gaa cgc gcg 307  
Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys Ala Leu Glu Arg Ala  
55 60 65  
aca atg aac cgc aca cga aaa gca cta tcg gat ctg gtg gat gca gct 355  
Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp Leu Val Asp Ala Ala  
70 75 80 85  
cca gaa act gca aca agg ctc aac gcg gat gac tca aca gag gta gtt 403  
Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp Ser Thr Glu Val Val  
90 95 100  
gag ctg tgg gag ctt gag ccc ggt gac atc gtc ttg gta cgc aat ggc 451  
Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val Leu Val Arg Asn Gly  
105 110 115  
gaa caa att ccc gtc gat gga aac gtg att gcg ggt gtc ggt gga att 499  
Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala Gly Val Gly Gly Ile  
120 125 130  
gat gaa tcc aac atc acg ggt gaa tca atg ccg gct gaa aag ggt caa 547  
Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro Ala Glu Lys Gly Gln  
135 140 145  
ggc tct gat gtg tat gca gga acc tgg ctg cga tct ggt gtt ttg aga 595

Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg Ser Gly Val Leu Arg	
150 155 160 165	
gtc gag gca aca gga att ggt tca gac tca act ttg gca aaa atc att	643
Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr Leu Ala Lys Ile Ile	
170 175 180	
cac cgc gtt gaa gac gcc cag gat gac aaa gcc cgc aca caa aca ttc	691
His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala Arg Thr Gln Thr Phe	
185 190 195	
tta gag aaa ttc tct aag tgg tac acc ccg ggc gtc atg atc gcc gcc	739
Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly Val Met Ile Ala Ala	
200 205 210	
gca gtg gtg gga ctt atc acc tgg gac gta gaa cta gca ctg acg ctc	787
Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu Leu Ala Leu Thr Leu	
215 220 225	
tta gtg atc ggc tgc ccc ggc gcg ttg gtt atc tcc atc ccg gtg tcc	835
Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile Ser Ile Pro Val Ser	
230 235 240 245	
atc gtc gca ggc atc ggc cgt gct gca cgc gat ggc gtg ctg atc aag	883
Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp Gly Val Leu Ile Lys	
250 255 260	
ggt gga gaa tac cta gaa acc gcc gcg aaa gtc gac gtc gtt gtc gtg	931
Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val Asp Val Val Val Val	
265 270 275	
gac aaa act gga acg ctg acc acc ggc cgc cca gaa ctc aca gac gta	979
Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro Glu Leu Thr Asp Val	
280 285 290	
gaa gtc atc gag ccc gcc tac agc cag ggc gag gtg ctg gag ctc gcc	1027
Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu Val Leu Glu Leu Ala	
295 300 305	
gcg cgc gcc gag acg gct tca gaa cat ccg ctt gcc gac gcc atc atc	1075
Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu Ala Asp Ala Ile Ile	
310 315 320 325	
cgt ggt gcc cag gat cgg ggg ctg tcc aca aca ttg gtg gaa gca gct	1123
Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr Leu Val Glu Ala Ala	
330 335 340	
gaa aac atc acc ggc cga ggc att atc gca aat gtt gat gga cag gca	1171
Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn Val Asp Gly Gln Ala	
345 350 355	
gtt gct gtt gga tct gct gag tta ctt gat cat gaa cca gac tcg acc	1219
Val Ala Val Gly Ser Ala Glu Leu Leu Asp His Glu Pro Asp Ser Thr	
360 365 370	
agg atc ctg gag cta aat gcc gaa gga aag acc gcg atg ttt gtc gga	1267
Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr Ala Met Phe Val Gly	
375 380 385	
gtg aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt	1315
Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg	

390	395	400	405	
tca gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa				1363
Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln				
	410	415	420	
gtt gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc				1411
Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala				
	425	430	435	
tcc aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag				1459
Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln				
	440	445	450	
aaa tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg				1507
Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala				
	455	460	465	
atg gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat				1555
Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Asp				
	470	475	480	485
atc gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc				1603
Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr				
	490	495	500	
gct gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca				1651
Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala				
	505	510	515	
gtg acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg				1699
Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu				
	520	525	530	
att gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc				1747
Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly				
	535	540	545	
gga gtt acc atg tcg gtt ggc atg ctc gtt cac gaa gca agc gtg ctg				1795
Gly Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu				
	550	555	560	565
ctt gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa				1843
Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu				
	570	575	580	
gat gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc				1891
Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu Ile Gln Gln Ile				
	585	590	595	
gca taaccaatgg ctgggtactg atg				1917
Ala				

&lt;210&gt; 398

&lt;211&gt; 598

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398



Met Leu Ala Asp Ala Phe Met Ile Ala Ala Ala Ile Val Ala Gly Trp  
 1 5 10 15  
 Pro Ile Ala Gln Ser Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser  
 20 25 30  
 Ile Asp Leu Leu Val Val Val Ala Ala Val Gly Ala Met Phe Ile Asn  
 35 40 45  
 Asn Tyr Trp Glu Ser Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys  
 50 55 60  
 Ala Leu Glu Arg Ala Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp  
 65 70 75 80  
 Leu Val Asp Ala Ala Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp  
 85 90 95  
 Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val  
 100 105 110  
 Leu Val Arg Asn Gly Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala  
 115 120 125  
 Gly Val Gly Gly Ile Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro  
 130 135 140  
 Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg  
 145 150 155 160  
 Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr  
 165 170 175  
 Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala  
 180 185 190  
 Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly  
 195 200 205  
 Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu  
 210 215 220  
 Leu Ala Leu Thr Leu Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile  
 225 230 235 240  
 Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp  
 245 250 255  
 Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val  
 260 265 270  
 Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro  
 275 280 285  
 Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu  
 290 295 300  
 Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu  
 305 310 315 320  
 Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr

325	330	335
Leu Val Glu Ala Ala Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn 340 345 350		
Val Asp Gly Gln Ala Val Ala Val Gly Ser Ala Glu Leu Leu Asp His 355 360 365		
Glu Pro Asp Ser Thr Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr 370 375 380		
Ala Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val 385 390 395 400		
Ala Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His 405 410 415		
Lys Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val 420 425 430		
Ala Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu 435 440 445		
Leu Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala 450 455 460		
Gly Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala 465 470 475 480		
Leu Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro 485 490 495		
Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro 500 505 510		
Arg Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met 515 520 525		
Arg Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala 530 535 540		
Gly Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His 545 550 555 560		
Glu Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg 565 570 575		
Pro Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser 580 585 590		
Glu Ile Gln Gln Ile Ala 595		

&lt;210&gt; 399

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(739)

&lt;223&gt; FRXA00980

&lt;400&gt; 399

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gaccaggatc ctggagctaa atgccgaagg aaagaccgcg atg ttt gtc gga gtg 115  
Met Phe Val Gly Val  
1 5

aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt tca 163  
Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg Ser  
10 15 20

gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa gtt 211  
Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln Val  
25 30 35

gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc tcc 259  
Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala Ser  
40 45 50

aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag aaa 307  
Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln Lys  
55 60 65

tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg atg 355  
Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala Met  
70 75 80 85

gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat atc 403  
Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp Ile  
90 95 100

gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc gct 451  
Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr Ala  
105 110 115

gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca gtg 499  
Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala Val  
120 125 130

acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg att 547  
Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu Ile  
135 140 145

gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc gga 595  
Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly Gly  
150 155 160 165

gtt acc atg tcg gtt ggc atg ctc gtt cac gaa gca agc gtg ctg ctt 643  
Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu Leu  
170 175 180

gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa gat 691  
Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu Asp  
185 190 195

gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc gca 739  
Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu Ile Gln Gln Ile Ala  
200 205 210

taaccaatgg ctgggtactg atg

762

<210> 400

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 400

Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala  
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Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys  
20 25 30

Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala  
35 40 45

Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu  
50 55 60

Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly  
65 70 75 80

Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu  
85 90 95

Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala  
100 105 110

Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg  
115 120 125

Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg  
130 135 140

Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly  
145 150 155 160

Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His Glu  
165 170 175

Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro  
180 185 190

Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu  
195 200 205

Ile Gln Gln Ile Ala  
210

<210> 401

<211> 2007

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1984)

<400> 401

<400> 401															60
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Met Leu Asn Arg Met															5
aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta															163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu															10
10 15 20															
ctc act ctc ggt gcc cta ggt gtt gtg ttc ggc gac atc ggc acc agc															211
Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser															25
30 35															
ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc															259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val															40
45 50															
gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg															307
Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp															55
60 65															
acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga															355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg															70
75 80 85															
gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg															403
Ala Asp Asn Gln Gly Gln Gly Ile Leu Ala Leu Val Ala Leu Leu															90
95 100															
aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg															451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu															105
110 115															
ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct															499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser															120
125 130															
gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag															547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu															135
140 145															
cgc ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca															595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala															150
155 160 165															
atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc															643
Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile															170
175 180															
atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc															691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile															185
190 195															
atc ggg cac cca gaa atc ttg cag agc ttg tct cca cat tgg gcc ctg															739
Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser Pro His Trp Ala Leu															200
205 210															

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg ctt ggt gcc Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu Leu Gly Ala 215 220 225	787
gtt gtc ctg aca gta acg ggt gcg gaa gcg ctc tac gct gat atg ggc Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu Tyr Ala Asp Met Gly 230 235 240 245	835
cat ttt ggg gcg agg cca atc aga gtg gcg tgg ttt tgc gtc gtc atg His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp Phe Cys Val Val Met 250 255 260	883
cct gct tta atc ttg acg tat ttg ggg cag ggc gcc ttg gtg atc aac Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn 265 270 275	931
cag cct gaa gcg gtg cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly 280 285 290	979
ctg cgg att ccg ttg gtt att ttg gcg acc atc gct acg gtg atc gca Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala 295 300 305	1027
tgc cag gcc gtg att tct ggt gcg tat tca ttg acc aag cag gcc gtg Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val 310 315 320 325	1075
aat ttg aaa ctg ctg cca cgc atg gtg atc cgg cat acc tcc cgc aaa Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg His Thr Ser Arg Lys 330 335 340	1123
gag gaa ggc cag atc tat atg cca ctg gtt aat gga ttg ctg ttt gta Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val 345 350 355	1171
tcc gtg atg gtt gtg gtg ctg gta ttc cga tcc tct gaa agc ctc gcc Ser Val Met Val Val Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala 360 365 370	1219
agc gcg tac gga ctt gca gtg acc gga acc ttg gtg ctg gtc agc gtc Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu Val Leu Val Ser Val 375 380 385	1267
ctg tat ctg atc tat gtt cac acc aca tgg tgg aaa aca gcg ctg ttc Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe 390 395 400 405	1315
att gtg ctc atc ggt att cca gaa gta ctt cta ttc gcc tcg aac acc Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr 410 415 420	1363
acg aaa att cac gac ggt ggc tgg ctt cca cta ctt att gcg gcc gtg Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val 425 430 435	1411
ctc atc gtg gtg atg cgg acc tgg gag tgg gga agt gac cgc gtc aat Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn 440 445 450	1459
cag gaa cgc gca gag ctg gaa ctt ccc atg gat aag ttc ttg gag aaa	1507

Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys  
 455 460 465  
 ctc gat cag cca cac aat att ggt ctg cgt aaa gtt gcc gaa gtg gca 1555  
 Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala  
 470 475 480 485  
 gta ttt cca cat ggc acc agc gat act gtc ccg ttg tca ttg gtt cgc 1603  
 Val Phe Pro His Gly Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg  
 490 495 500  
 tgc gtg aaa gac ctc aag ctt tta tac cga gag atc gtg atc gtt cga 1651  
 Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg  
 505 510 515  
 atc gtc caa gaa cac gtt ccg cac gtg cca cca gag gaa cgc gcg gaa 1699  
 Ile Val Gln Glu His Val Pro His Val Pro Pro Glu Glu Arg Ala Glu  
 520 525 530  
 atg gaa gtg ctc cat cac gcc ccg atc aga gtc gtg cga gtt gat ctg 1747  
 Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu  
 535 540 545  
 cac ctt ggt tat ttt gat gag cag aac ctg cct gag cat ctc cat gcc 1795  
 His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala  
 550 555 560 565  
 att gac cca aca tgg gat aac gcc acc tac ttc ctg tct gcc ctg act 1843  
 Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr  
 570 575 580  
 ctt cgg agc agg ttg cct gga aag att gct ggc tgg cgt gat cgt ttg 1891  
 Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu  
 585 590 595  
 tat ctt tgg atg gaa cgt aat cag gca tct cga act gag tct ttc aaa 1939  
 Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys  
 600 605 610  
 ttg caa cca agc aaa acc atc acg gtt gga aca gag ctg cac ctt 1984  
 Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr Glu Leu His Leu  
 615 620 625  
 taatcaggca gttgctggcc aac 2007

&lt;210&gt; 402

&lt;211&gt; 628

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Leu Asn Arg Met Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys  
 1 5 10 15

Ser Gly Gln Ala Leu Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly  
 20 25 30

Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met  
 35 40 45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile  
 50 55 60  
 Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val  
 65 70 75 80  
 Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala  
 85 90 95  
 Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala  
 100 105 110  
 Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile  
 115 120 125  
 Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile  
 130 135 140  
 Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu  
 145 150 155 160  
 Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys  
 165 170 175  
 Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu  
 180 185 190  
 Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser  
 195 200 205  
 Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe  
 210 215 220  
 Val Leu Leu Gly Ala Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu  
 225 230 235 240  
 Tyr Ala Asp Met Gly His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp  
 245 250 255  
 Phe Cys Val Val Met Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly  
 260 265 270  
 Ala Leu Val Ile Asn Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr  
 275 280 285  
 Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile  
 290 295 300  
 Ala Thr Val Ile Ala Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu  
 305 310 315 320  
 Thr Lys Gln Ala Val Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg  
 325 330 335  
 His Thr Ser Arg Lys Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn  
 340 345 350  
 Gly Leu Leu Phe Val Ser Val Met Val Val Val Leu Val Phe Arg Ser  
 355 360 365  
 Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu



370	375	380
Val Leu Val Ser Val Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp 385 390 395 400		
Lys Thr Ala Leu Phe Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu 405 410 415		
Phe Ala Ser Asn Thr Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu 420 425 430		
Leu Ile Ala Ala Val Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly 435 440 445		
Ser Asp Arg Val Asn Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp 450 455 460		
Lys Phe Leu Glu Lys Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys 465 470 475 480		
Val Ala Glu Val Ala Val Phe Pro His Gly Thr Ser Asp Thr Val Pro 485 490 495		
Leu Ser Leu Val Arg Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu 500 505 510		
Ile Val Ile Val Arg Ile Val Gln Glu His Val Pro His Val Pro Pro 515 520 525		
Glu Glu Arg Ala Glu Met Glu Val Leu His His Ala Pro Ile Arg Val 530 535 540		
Val Arg Val Asp Leu His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro 545 550 555 560		
Glu His Leu His Ala Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe 565 570 575		
Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly 580 585 590		
Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg 595 600 605		
Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr 610 615 620		
Glu Leu His Leu 625		

&lt;210&gt; 403

&lt;211&gt; 1157

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1134)

&lt;223&gt; FRXA02348

&lt;400&gt; 403

cca atc aga gtg gcg tgg ttt tgc gtc gtc atg cct gct tta atc ttg	48
Pro Ile Arg Val Ala Trp Phe Cys Val Val Met Pro Ala Leu Ile Leu	
1 5 10 15	
acg tat ttg ggg cag ggc gcc ttg gtg atc aac cag cct gaa gcg gtg	96
Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val	
20 25 30	
cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt ctg cgg att ccg ttg	144
Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu	
35 40 45	
gtt att ttg gcg acc atc got acg gtg atc gca tcg cag gcc gtg att	192
Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile	
50 55 60	
tct ggt gcg tat tca ttg acc aag cag gcc gtg aat ttg aaa ctg ctg	240
Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu	
65 70 75 80	
cca cgc atg gtg atc cgg cat acc tcc cgc aaa gag gaa ggc cag atc	288
Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile	
85 90 95	
tat atg cca ctg gtt aat gga ttg ctg ttt gta tcc gtg atg gtt gtg	336
Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val	
100 105 110	
gtg ctg gta ttc cga tcc tct gaa agc ctc gcc agc gcg tac gga ctt	384
Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu	
115 120 125	
gca gtg acc gga acc ttg gtg ctg gtc agc gtc ctg tat ctg atc tat	432
Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr	
130 135 140	
gtt cac acc aca tgg tgg aaa aca gcg ctg ttc att gtg ctc atc ggt	480
Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly	
145 150 155 160	
att cca gaa gta ctt cta ttc gcc tcg aac acc acg aaa att cac gac	528
Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp	
165 170 175	
ggt ggc tgg ctt cca cta ctt att gcg gcc gtg ctc atc gtg gtg atg	576
Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met	
180 185 190	
cgg acc tgg gag tgg gga agt gac cgc gtc aat cag gaa cgc gca gag	624
Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu	
195 200 205	
ctg gaa ctt ccc atg gat aag ttc ttg gag aaa ctc gat cag cca cac	672
Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His	
210 215 220	
aat att ggt ctg cgt aaa gtt gcc gaa gtg gca gta ttt cca cat ggc	720
Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly	
225 230 235 240	

acc agc gat act gtc ccg ttg tca ttg gtt cgc tgc gtg aaa gac ctc 768  
 Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu  
 245 250 255

aag ctt tta tac cga gag atc gtg atc gtt cga atc gtc caa gaa cac 816  
 Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His  
 260 265 270

gtt ccg cac gtg cca cca gag gaa cgc gcg gaa atg gaa gtg ctc cat 864  
 Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His  
 275 280 285

cac gcc ccg atc aga gtc gtg cga gtt gat ctg cac ctt ggt tat ttt 912  
 His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe  
 290 295 300

gat gag cag aac ctg cct gag cat ctc cat gcc att gac cca aca tgg 960  
 Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp  
 305 310 315 320

gat aac gcc acc tac ttc ctg tct gcc ctg act ctt cgg agc agg ttg 1008  
 Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu  
 325 330 335

cct gga aag att gct ggc tgg cgt gat cgt ttg tat ctt tcg atg gaa 1056  
 Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu  
 340 345 350

cgt aat cag gca tct cga act gag tct ttc aaa ttg caa cca agc aaa 1104  
 Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys  
 355 360 365

acc atc acg gtt gga aca gag ctg cac ctt taatcaggca gttgctggcc 1154  
 Thr Ile Thr Val Gly Thr Glu Leu His Leu  
 370 375

aac 1157

&lt;210&gt; 404

&lt;211&gt; 378

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

Pro Ile Arg Val Ala Trp Phe Cys Val Val Met Pro Ala Leu Ile Leu  
 1 5 10 15

Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val  
 20 25 30

Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu  
 35 40 45

Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile  
 50 55 60

Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu  
 65 70 75 80

Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile

85	90	95
Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val 100 105 110		
Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu 115 120 125		
Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr 130 135 140		
Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly 145 150 155 160		
Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp 165 170 175		
Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met 180 185 190		
Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu 195 200 205		
Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His 210 215 220		
Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly 225 230 235 240		
Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu 245 250 255		
Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His 260 265 270		
Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His 275 280 285		
His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe 290 295 300		
Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp 305 310 315 320		
Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu 325 330 335		
Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu 340 345 350		
Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys 355 360 365		
Thr Ile Thr Val Gly Thr Glu Leu His Leu 370 375		

&lt;210&gt; 405

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<400>	405
aagacccga gccgaagccc tggcctgcgc atacttcctt gtcaacgctc gctgggatta	60
ggtcttttct gagcgctagc atttctccac tcaaaggagc atg ctt aac cgc atg Met Leu Asn Arg Met	115
	1                5
aaa agt gcg cgG cca aaa tca gtc gct cca aaa tcc gga caa gct tta	163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu	
	10            15            20
ctc act ctC ggt gcc cta ggt gtt gtg ttC ggC gac atC ggC acc agC	211
Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser	
	25                30            35
ccc ctg tac tca ctt cac act gca ttC agC atg cag cac aac aaa gtc	259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val	
	40            45            50
gaa gtc act cag gaa aaT gtg tac ggC atC atC tcC atg gtg ttg tgg	307
Glu Val Thr Gln GlU Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp	
	55                60            65
acc atC act ttg atC gtc acc gtc aaa tac gtc atg ctg gtc acc cga	355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg	
	70            75            80            85
gct gac aac caa gga caa ggt ggC atC ctg gcg ctC gtt gct ttg ctg	403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu	
	90                95            100
aaa aac cgT ggg cac tgg gga aaa ttC gtg gca gta gcc ggC atg ttg	451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu	
	105            110            115
ggC gcc gca ttg ttt tat ggC gat gtg gtg atC acc ccg gcg atC tct	499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser	
	120            125            130
gtt ctC agC gca aca gaA ggC ttg acg gtt atC tcC cca agC ttt gag	547
Val Leu Ser Ala Thr GlU Gly Leu Thr Val Ile Ser Pro Ser Phe GlU	
	135            140            145
cgc ttC att ctg ccc gta tct ctC gca gtt ctg atC gct att ttt gca	595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala	
	150            155            160            165
atC caa ccg ctC ggt aca gaA aaA gtc ggC aaA gcc ttC ggC ccc atC	643
Ile Gln Pro Leu Gly Thr GlU Lys Val Gly Lys Ala Phe Gly Pro Ile	
	170            175            180
atg ttg ctg tgg ttt gtc acc ctT gca gga ttg gga att ccg caa atC	691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile	
	185            190            195

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg 778  
Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu  
215 220 225

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<210> 406
<211> 226
<212> PRT
<213> Corynebacterium glutamicum
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<400> 406

Met Leu Asn Arg Met Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys  
1 5 10 15

Ser Gly Gln Ala Leu Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly  
20 25 30

Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met  
35 40 45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile  
50 55 60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val  
65 70 75 80

Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala  
85 90 95

Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala  
100 105 110

Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile  
115 120 125

Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile  
130 135 140

Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu  
145 150 155 160

Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys  
165 170 175

Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu  
180 185 190

Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser  
195 200 205

Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe  
210 215 220

Val Leu  
225

<210> 407  
 <211> 1058  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1035)  
 <223> RXN00960

<400> 407  
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 Met Ala Arg His Cys Cys Ser Asn Arg Tyr Ala Ser Thr Val Phe Ser  
 1 5 10 15  
 ggt ctg atc gcc tac gga gca tcc caa gcg ctc tac cca tgg ctg ctg 96  
 Gly Leu Ile Ala Tyr Gly Ala Ser Gln Ala Leu Tyr Pro Trp Leu Leu  
 20 25 30  
 aaa gac cac caa agc gtc acc gaa atc gac ctt gat gca ggt gcc ctc 144  
 Lys Asp His Gln Ser Val Thr Glu Ile Asp Leu Asp Ala Gly Ala Leu  
 35 40 45  
 cag ccc tac ttc aac atc gag atg cca cca cca ttt gaa gtg atg acc 192  
 Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Phe Glu Val Met Thr  
 50 55 60  
 gca ctg ctg ctg gca ttc tgc ctc ggc ctg ggc atg gct gta att aaa 240  
 Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys  
 65 70 75 80  
 tca gac acc ctg ttc aag gta acc cgc gaa ctc gag cgc gta gtc atg 288  
 Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met  
 85 90 95  
 aag acc atc acc gcc ttt gtc atc cca ctg ctg cca ctc ttc atc ttc 336  
 Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe  
 100 105 110  
 ggc atc ttc ctc ggc atg ggc atg aac ggt ggc ctc ctg gag atc atg 384  
 Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Glu Ile Met  
 115 120 125  
 tcc gcc ttt ggc aag gta ctg att ctc gcc gtc gtg gga acc ctg ctc 432  
 Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu  
 130 135 140  
 ttc cta gcc atc cag ttc att atc gct ggt gca gta tcc aag aag aac 480  
 Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn  
 145 150 155 160  
 cca tgg aaa ctg ttc aaa aac atg ctc cct gca tac ttc act gca ctg 528  
 Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu  
 165 170 175  
 ggc act tcc tct tca gcg gca acc atc cca gtg acc tac cag cag acc 576  
 Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr  
 180 185 190  
 ctg aaa aac gat gtt gat gtc aac gtc gca ggc ttt gtt gtc cca ctg 624  
 Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu

195	200	205	
tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc			672
Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe			
210	215	220	
acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc			720
Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu			
225	230	235	240
tcc atc gga ttc ctc ctc atg ctg ggc atc acc atg atc gcc gca cca			768
Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro			
	245	250	255
ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc			816
Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser			
	260	265	270
atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac			864
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr			
	275	280	285
atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc			912
Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly			
	290	295	300
gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc			960
Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr			
305	310	315	320
act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc			1008
Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile			
	325	330	335
act cca tcg gat gtg gaa cat cac aag tagaaacccg cattttctgt agt			1058
Thr Pro Ser Asp Val Glu His His Lys			
	340	345	

&lt;210&gt; 408

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Met	Ala	Arg	His	Cys	Cys	Ser	Asn	Arg	Tyr	Ala	Ser	Thr	Val	Phe	Ser
1				5					10					15	

Gly	Leu	Ile	Ala	Tyr	Gly	Ala	Ser	Gln	Ala	Leu	Tyr	Pro	Trp	Leu	Leu
		20						25					30		

Lys	Asp	His	Gln	Ser	Val	Thr	Glu	Ile	Asp	Leu	Asp	Ala	Gly	Ala	Leu
		35					40					45			

Gln	Pro	Tyr	Phe	Asn	Ile	Glu	Met	Pro	Pro	Pro	Phe	Glu	Val	Met	Thr
	50					55					60				

Ala	Leu	Leu	Leu	Ala	Phe	Cys	Leu	Gly	Leu	Gly	Met	Ala	Val	Ile	Lys
65					70					75					80

Ser	Asp	Thr	Leu	Phe	Lys	Val	Thr	Arg	Glu	Leu	Glu	Arg	Val	Val	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



85	90	95
Lys Thr Ile Thr Ala Phe Val Ile	Pro Leu Leu Pro Leu	Phe Ile Phe
100	105	110
Gly Ile Phe Leu Gly Met Gly Met	Asn Gly Gly Leu Leu	Glu Ile Met
115	120	125
Ser Ala Phe Gly Lys Val Leu Ile	Leu Ala Val Val Gly Thr Leu Leu	
130	135	140
Phe Leu Ala Ile Gln Phe Ile Ile	Ala Gly Ala Val Ser Lys Lys Asn	
145	150	155
Pro Trp Lys Leu Phe Lys Asn Met	Leu Pro Ala Tyr Phe Thr Ala Leu	
165	170	175
Gly Thr Ser Ser Ser Ala Ala Thr	Ile Pro Val Thr Tyr Gln Gln Thr	
180	185	190
Leu Lys Asn Asp Val Asp Val Asn	Val Ala Gly Phe Val Val Pro Leu	
195	200	205
Cys Ala Thr Ile His Leu Ala Gly	Ser Met Met Lys Ile Gly Leu Phe	
210	215	220
Thr Phe Ala Val Val Phe Met Tyr	Asp Met Glu Val Gly Val Gly Leu	
225	230	235
Ser Ile Gly Phe Leu Leu Met Leu	Gly Ile Thr Met Ile Ala Ala Pro	
245	250	255
Gly Val Pro Gly Gly Ala Ile Met	Ala Ala Thr Gly Met Leu Ala Ser	
260	265	270
Met Leu Gly Phe Asn Thr Glu Gln	Val Ala Leu Met Ile Ala Ala Tyr	
275	280	285
Ile Ala Ile Asp Ser Phe Gly Thr	Ala Ala Asn Val Thr Gly Asp Gly	
290	295	300
Ala Ile Ala Val Ile Val Asn Lys	Phe Ala Lys Gly Gln Leu His Thr	
305	310	315
Thr Ser Pro Asp Glu Ile Glu Glu	Asp Asp Arg Val Ala Phe Asp Ile	
325	330	335
Thr Pro Ser Asp Val Glu His His	Lys	
340	345	

&lt;210&gt; 409

&lt;211&gt; 482

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(459)

&lt;223&gt; FRXA00960

&lt;400&gt; 409

ctg	aaa	aac	gat	gtt	gat	gtc	aac	gtc	gca	ggc	ttt	gtt	gtc	cca	ctg	48
Leu	Lys	Asn	Asp	Val	Asp	Val	Asn	Val	Ala	Gly	Phe	Val	Val	Pro	Leu	
1				5					10					15		
tgc	gcc	acc	atc	cac	cta	gct	gga	tcg	atg	atg	aag	atc	ggc	ctc	ttc	96
Cys	Ala	Thr	Ile	His	Leu	Ala	Gly	Ser	Met	Met	Lys	Ile	Gly	Leu	Phe	
			20					25					30			
acc	ttc	gct	gtt	gtc	ttc	atg	tac	gac	atg	gaa	gta	ggc	gtc	ggc	ctc	144
Thr	Phe	Ala	Val	Val	Phe	Met	Tyr	Asp	Met	Glu	Val	Gly	Val	Gly	Leu	
		35					40					45				
tcc	atc	gga	ttc	ctc	ctc	atg	ctg	ggc	atc	acc	atg	atc	gcc	gca	cca	192
Ser	Ile	Gly	Phe	Leu	Leu	Met	Leu	Gly	Ile	Thr	Met	Ile	Ala	Ala	Pro	
	50					55					60					
ggc	gtt	ccc	ggc	gga	gcc	atc	atg	gca	gca	acc	ggc	atg	ctg	gcc	tcc	240
Gly	Val	Pro	Gly	Gly	Ala	Ile	Met	Ala	Ala	Thr	Gly	Met	Leu	Ala	Ser	
65				70						75				80		
atg	ctc	gga	ttc	aac	acc	gaa	caa	gtc	gcc	ctc	atg	atc	gcc	gct	tac	288
Met	Leu	Gly	Phe	Asn	Thr	Glu	Gln	Val	Ala	Leu	Met	Ile	Ala	Ala	Tyr	
				85				90						95		
atc	gcg	att	gac	tcc	ttc	ggc	acc	gca	gca	aac	gtc	acc	ggc	gac	ggc	336
Ile	Ala	Ile	Asp	Ser	Phe	Gly	Thr	Ala	Ala	Asn	Val	Thr	Gly	Asp	Gly	
			100					105					110			
gca	atc	gca	gtc	atc	gtg	aac	aaa	ttc	gcc	aag	ggc	cag	ctg	cac	acc	384
Ala	Ile	Ala	Val	Ile	Val	Asn	Lys	Phe	Ala	Lys	Gly	Gln	Leu	His	Thr	
		115				120						125				
act	tcc	cca	gat	gaa	atc	gaa	gaa	gac	gac	cgc	gtt	gcc	ttc	gac	atc	432
Thr	Ser	Pro	Asp	Glu	Ile	Glu	Glu	Asp	Asp	Arg	Val	Ala	Phe	Asp	Ile	
	130					135				140						
act	cca	tcg	gat	gtg	gaa	cat	cac	aag	tagaaa	ccccg	cattttt	ctgt				479
Thr	Pro	Ser	Asp	Val	Glu	His	His	Lys								
145					150											
agt																482

&lt;210&gt; 410

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Leu	Lys	Asn	Asp	Val	Asp	Val	Asn	Val	Ala	Gly	Phe	Val	Val	Pro	Leu	
1				5					10					15		
Cys	Ala	Thr	Ile	His	Leu	Ala	Gly	Ser	Met	Met	Lys	Ile	Gly	Leu	Phe	
			20					25					30			
Thr	Phe	Ala	Val	Val	Phe	Met	Tyr	Asp	Met	Glu	Val	Gly	Val	Gly	Leu	
		35					40					45				
Ser	Ile	Gly	Phe	Leu	Leu	Met	Leu	Gly	Ile	Thr	Met	Ile	Ala	Ala	Pro	
	50					55					60					

Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser  
 65 70 75 80  
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr  
 85 90 95  
 Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly  
 100 105 110  
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr  
 115 120 125  
 Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile  
 130 135 140  
 Thr Pro Ser Asp Val Glu His His Lys  
 145 150

<210> 411  
 <211> 1509  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1486)  
 <223> RXA01070

<400> 411  
 cagcttcggt taatttggtc aactaatgc aataaattcc tgtctacagc gttacagtta 60  
 atgaattcaa ttcaaccgct aaacgcaagg agtgctaccc atg gct aac gcc acc 115  
 Met Ala Asn Ala Thr  
 1 5  
 gca cag aag ggc cgt ttc ggc ctt ccc ggc tgg atg act ggc ttt ggt 163  
 Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp Met Thr Gly Phe Gly  
 10 15 20  
 gcc cag gtt atc gcc ggc ctc att ctt ggt ctt att ctc ggc ctt gtc 211  
 Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu Ile Leu Gly Leu Val  
 25 30 35  
 gcc cga ggc atg gac agc ggc gct gca gac ggt gaa gca agc tgg ctt 259  
 Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly Glu Ala Ser Trp Leu  
 40 45 50  
 acc ggt ctt ctt agc ggc gtc ggt tct gct tat gtt tct cta ctt aaa 307  
 Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr Val Ser Leu Leu Lys  
 55 60 65  
 gtt atg gtt cca cca ctg gtg ttc gct gca gtg gtt acc agt gtg gca 355  
 Val Met Val Pro Pro Leu Val Phe Ala Ala Val Val Thr Ser Val Ala  
 70 75 80 85  
 aag ttg cgc gag gta gct aac gct gct cgc ctg gct gtt tcc acc ttg 403  
 Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu Ala Val Ser Thr Leu  
 90 95 100

gtg tgg ttc gcc att act gca ttc ttc tct gtg ctc gcg ggt atc gcc Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val Leu Ala Gly Ile Ala 105 110 115	451
gta gcg ctg att atg cag cct ggt gtt gga tcc act gtc gac gca tct Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser Thr Val Asp Ala Ser 120 125 130	499
aat gct gct gat cct tct cgc gtg ggc agc tgg ctg ggc ttt atc cag Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp Leu Gly Phe Ile Gln 135 140 145	547
tcc gtt att cca tca aac att ctg gga ctt tcc ggt tct tac agt gag Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser Gly Ser Tyr Ser Glu 150 155 160 165	595
aac tct ggt gtg aac ctg tcc ttc aac gtg ctg cag atc ctg gtt atc Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu Gln Ile Leu Val Ile 170 175 180	643
tcc att gcg att ggt gtt gca gct ctg aag gct ggc aag tcc gcc gag Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala Gly Lys Ser Ala Glu 185 190 195	691
cct ttc ttg aag ttc acc gag tcc ttc ctc aag atc atc cag atc gtg Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys Ile Ile Gln Ile Val 200 205 210	739
ttg tgg tgg att att cgc ctg gct cca att ggt tcc gct gcg ctg atc Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly Ser Ala Ala Leu Ile 215 220 225	787
ggt aat gct gtt gct acc tac ggt tgg tct gca ctt gga tcc ctg ggc Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala Leu Gly Ser Leu Gly 230 235 240 245	835
aag ttt gtt ctt gcg atc tac gtt ggt ctg gca atc gtc atg ttc gtt Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala Ile Val Met Phe Val 250 255 260	883
atc tac cca gtc gtg ctg aag ctc aat gga att cct gtt ctt gga ttc Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile Pro Val Leu Gly Phe 265 270 275	931
ttc aag cgc gtt tgg cct gtc aca agc ctt ggc ttt gtt acc cgt tcc Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly Phe Val Thr Arg Ser 280 285 290	979
tcc atg ggc gtt atg cca gtt acc cag cgc gtt act gag cag tcc ttg Ser Met Gly Val Met Pro Val Thr Gln Arg Val Thr Glu Gln Ser Leu 295 300 305	1027
ggt gtt cca tct gcg tac gct tcc ttt gct atc cca ctg ggt gcg acc Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile Pro Leu Gly Ala Thr 310 315 320 325	1075
agc aag atg gac ggc tgc gct gct gtc tac cca gct gtt gcc gct atc Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro Ala Val Ala Ala Ile 330 335 340	1123
ttc gtg gca cag ttc tac ggc att gac ttg agc atc atg gat tac gta	1171

Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser Ile Met Asp Tyr Val  
 345 350 355  
 ctg atc atg atc gtc tct gtc ctg ggc tct gct gca act gca ggc acc 1219  
 Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala Ala Thr Ala Gly Thr  
 360 365 370  
 act ggc gca acc gtc atg ctg acc ctg acc cta tcc acc ttg ggt ctg 1267  
 Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu Ser Thr Leu Gly Leu  
 375 380 385  
 cca ctt gct ggt gtt ggt ctg ctg ctg gct atc gag cca atc atc gac 1315  
 Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile Glu Pro Ile Ile Asp  
 390 395 400 405  
 atg gga cgt acc gca acc aac gtc acc ggt cag gca ctg gtt cct gcg 1363  
 Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln Ala Leu Val Pro Ala  
 410 415 420  
 atc gtt gct aag cgc gag ggc att ctg gat cag gat gtg tgg gat gct 1411  
 Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln Asp Val Trp Asp Ala  
 425 430 435  
 gct gaa aag ggt ggc gct gct att gaa atg gca acc gtc tct gag aaa 1459  
 Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala Thr Val Ser Glu Lys  
 440 445 450  
 gaa act gag cct gca gag gtt cgc tcc taagctctct tgagtacctg aga 1509  
 Glu Thr Glu Pro Ala Glu Val Arg Ser  
 455 460

&lt;210&gt; 412

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Met Ala Asn Ala Thr Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp  
 1 5 10 15

Met Thr Gly Phe Gly Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu  
 20 25 30

Ile Leu Gly Leu Val Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly  
 35 40 45

Glu Ala Ser Trp Leu Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr  
 50 55 60

Val Ser Leu Leu Lys Val Met Val Pro Pro Leu Val Phe Ala Ala Val  
 65 70 75 80

Val Thr Ser Val Ala Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu  
 85 90 95

Ala Val Ser Thr Leu Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val  
 100 105 110

Leu Ala Gly Ile Ala Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser  
 115 120 125

Thr Val Asp Ala Ser Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp  
 130 135 140

Leu Gly Phe Ile Gln Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser  
 145 150 155 160

Gly Ser Tyr Ser Glu Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu  
 165 170 175

Gln Ile Leu Val Ile Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala  
 180 185 190

Gly Lys Ser Ala Glu Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys  
 195 200 205

Ile Ile Gln Ile Val Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly  
 210 215 220

Ser Ala Ala Leu Ile Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala  
 225 230 235 240

Leu Gly Ser Leu Gly Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala  
 245 250 255

Ile Val Met Phe Val Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile  
 260 265 270

Pro Val Leu Gly Phe Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly  
 275 280 285

Phe Val Thr Arg Ser Ser Met Gly Val Met Pro Val Thr Gln Arg Val  
 290 295 300

Thr Glu Gln Ser Leu Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile  
 305 310 315 320

Pro Leu Gly Ala Thr Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro  
 325 330 335

Ala Val Ala Ala Ile Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser  
 340 345 350

Ile Met Asp Tyr Val Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala  
 355 360 365

Ala Thr Ala Gly Thr Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu  
 370 375 380

Ser Thr Leu Gly Leu Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile  
 385 390 395 400

Glu Pro Ile Ile Asp Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln  
 405 410 415

Ala Leu Val Pro Ala Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln  
 420 425 430

Asp Val Trp Asp Ala Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala  
 435 440 445

Thr Val Ser Glu Lys Glu Thr Glu Pro Ala Glu Val Arg Ser  
 450 455 460

<210> 413  
 <211> 428  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(405)  
 <223> RXA02628

<400> 413  
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 Met Leu Glu Gly Phe Arg Asp Phe Val Leu Arg Gly Asn Val Ile Glu  
 1 5 10 15  
 ctc gca gtt gcc gtg gtc atc ggt act gcc ttc acc gct atc gtg aca 96  
 Leu Ala Val Ala Val Val Ile Gly Thr Ala Phe Thr Ala Ile Val Thr  
 20 25 30  
 gca ttc tcc gag agc atc atc aac cca ttg atc gct tcc atc ggc agc 144  
 Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser  
 35 40 45  
 aca gag gtt gaa ggc ctc ggc ttc cac atc cgc gcc ggc aat gcc gca 192  
 Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala  
 50 55 60  
 aca ttc gtg gat ttt ggt gct gtc atc acc gca gcg atc aac ttc ctc 240  
 Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu  
 65 70 75 80  
 atc atc gca gca att gtc tac ttc gtt ctc gtt gct cca atg aac aag 288  
 Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys  
 85 90 95  
 ctc agc gaa acc ctc gca aag cgc aag ggt gtt gaa gaa gac gag acc 336  
 Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr  
 100 105 110  
 cca gct tcc atc gaa gca gaa ctc ctc acc gag atc cgc gat ctc ctg 384  
 Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu  
 115 120 125  
 cag gag caa aag cgc ctt cag tagttaaag gccctaaaag cac 428  
 Gln Glu Gln Lys Arg Leu Gln  
 130 135

<210> 414  
 <211> 135  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 414  
 Met Leu Glu Gly Phe Arg Asp Phe Val Leu Arg Gly Asn Val Ile Glu  
 1 5 10 15

Leu Ala Val Ala Val Val Ile Gly Thr Ala Phe Thr Ala Ile Val Thr  
                   20                  25                  30  
 Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser  
           35                  40                  45  
 Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala  
       50                  55                  60  
 Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu  
       65                  70                  75                  80  
 Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys  
                   85                  90                  95  
 Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr  
           100                  105                  110  
 Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu  
           115                  120                  125  
 Gln Glu Gln Lys Arg Leu Gln  
       130                  135

<210> 415  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(970)  
 <223> RXN03164

<400> 415  
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 tgtcatggca tatcaaccag cagacaatcg ctatgacgac atg atc tac cgc agg 115  
   Met Ile Tyr Arg Arg  
   1                  5  
 gtg gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg 163  
 Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp  
                   10                  15                  20  
 cac aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att 211  
 His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile  
                   25                  30                  35  
 cac cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac 259  
 His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn  
           40                  45                  50  
 tat gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg 307  
 Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu  
       55                  60                  65  
 cgt gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag 355  
 Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys  
       70                  75                  80                  85



gcg ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga 403  
Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg  
90 95 100

aag tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg 451  
Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu  
105 110 115

gat tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct 499  
Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro  
120 125 130

ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag 547  
Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys  
135 140 145

gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag 595  
Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu  
150 155 160 165

gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag 643  
Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln  
170 175 180

cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac 691  
Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp  
185 190 195

ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att 739  
Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile  
200 205 210

gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat 787  
Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp  
215 220 225

gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctg tct gag 835  
Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Leu Ser Glu  
230 235 240 245

ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag ctc aat gac 883  
Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys Leu Asn Asp  
250 255 260

atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg ctt gca tgg 931  
Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala Leu Ala Trp  
265 270 275

gtg ctg cgc gag caa aga gag tac ggc gcc gga tta ccg tgaccagtgc 980  
Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly Leu Pro  
280 285 290

attgattggt gct 993

&lt;210&gt; 416

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

Met Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile  
 1 5 10 15  
 Ser Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr  
 20 25 30  
 Gln Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe  
 35 40 45  
 Asp Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn  
 50 55 60  
 Phe Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu  
 65 70 75 80  
 Ile Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly  
 85 90 95  
 Phe Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu  
 100 105 110  
 Thr Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro  
 115 120 125  
 Asp Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile  
 130 135 140  
 Val Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro  
 145 150 155 160  
 Glu Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro  
 165 170 175  
 Leu Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu  
 180 185 190  
 Glu Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn  
 195 200 205  
 Gly Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr  
 210 215 220  
 Asp Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly  
 225 230 235 240  
 Lys Ser Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val  
 245 250 255  
 Arg Lys Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln  
 260 265 270  
 Met Ala Leu Ala Trp Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly  
 275 280 285  
 Leu Pro  
 290

&lt;210&gt; 417

&lt;211&gt; 1209

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1186)

&lt;223&gt; FRXA01395

&lt;220&gt;

&lt;223&gt; All occurrences of n = any nucleotide

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 417

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ctcaaaagca ctgataaaag cagtcaaccc acctcgggtt ggctgctttt ttgcatccag 60

atgcacaaag ccgtggcaca aacgagacaa actgagcaca atg gct gtc atg gca 115
                                         Met Ala Val Met Ala
                                         1 5

tat caa cca gca gac aat cgc tat gac gac atg atc tac cgc agg gtg 163
Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met Ile Tyr Arg Arg Val
                        10 15 20

gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg cac 211
Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp His
                        25 30 35

aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att cac 259
Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile His
                        40 45 50

cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac tat 307
Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn Tyr
                        55 60 65

gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg cgt 355
Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu Arg
                        70 75 80 85

gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag gcg 403
Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys Ala
                        90 95 100

ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga aag 451
Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg Lys
                        105 110 115

tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg gat 499
Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu Asp
                        120 125 130

tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct ttg 547
Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro Leu
                        135 140 145

gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag gct 595
Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys Ala
                        150 155 160 165

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ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag gcg 643  
 Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu Ala  
 170 175 180

gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag cca 691  
 Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln Pro  
 185 190 195

agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac ggt 739  
 Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp Gly  
 200 205 210

gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att gct 787  
 Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile Ala  
 215 220 225

ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat gga 835  
 Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp Gly  
 230 235 240 245

att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctk tst kac ggs 883  
 Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Xaa Xaa Xaa Xaa  
 250 255 260

wtg ttg aac gtg aac aat att gat wtg gtc ccm ars ytn awk rsa wtt 931  
 Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa  
 265 270 275

tcc mar ram acc ggg cag tcc ttt nnc cna aag gnc ttt tgt tgg gtt 979  
 Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys Xaa Phe Cys Trp Val  
 280 285 290

gtt gcc caa cca agg aaa gta cgg cgc cgg att acc gtg acc agt gca 1027  
 Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile Thr Val Thr Ser Ala  
 295 300 305

ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc ctt gat tca 1075  
 Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser Leu Asp Ser  
 310 315 320 325

ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg atc gat gag 1123  
 Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala Ile Asp Glu  
 330 335 340

att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc acc gat tcc 1171  
 Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala Thr Asp Ser  
 345 350 355

aaa acc cgc gaa aac taacccatca acatcagttt gat 1209  
 Lys Thr Arg Glu Asn  
 360

&lt;210&gt; 418

&lt;211&gt; 362

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 418

Met Ala Val Met Ala Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met  
 1 5 10 15  
 Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser  
 20 25 30  
 Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln  
 35 40 45  
 Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp  
 50 55 60  
 Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe  
 65 70 75 80  
 Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile  
 85 90 95  
 Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe  
 100 105 110  
 Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr  
 115 120 125  
 Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp  
 130 135 140  
 Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val  
 145 150 155 160  
 Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu  
 165 170 175  
 Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu  
 180 185 190  
 Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu  
 195 200 205  
 Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly  
 210 215 220  
 Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp  
 225 230 235 240  
 Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys  
 245 250 255  
 Ser Xaa Xaa Xaa Xaa Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa  
 260 265 270  
 Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys  
 275 280 285  
 Xaa Phe Cys Trp Val Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile  
 290 295 300  
 Thr Val Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp  
 305 310 315 320

Asn Ser Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu  
325 330 335

Glu Ala Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala  
340 345 350

Lys Ala Thr Asp Ser Lys Thr Arg Glu Asn  
355 360

<210> 419

<211> 1911

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1888)

<223> RXA02597

<400> 419

ataccacatt tgcaagaatt acaaacgggg gcaccctcaa tgacttgaaa cactttatag 60

agtagaaagt gagtcacgac actttttaaa ggaggatgct ttg ccc gaa caa gac 115  
Leu Pro Glu Gln Asp  
1 5

tta acc acc ttg gcc aat gat tgg ctc caa gct ttt gaa aag gcc act 163  
Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala Phe Glu Lys Ala Thr  
10 15 20

gct agt tcc agc cct gat gaa gct gcc act gca gtc gtg caa ctt ttt 211  
Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala Val Val Gln Leu Phe  
25 30 35

gag gat gaa gga tac tgg cga gac ctt ctt gca ttc acg tgg aac ctc 259  
Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala Phe Thr Trp Asn Leu  
40 45 50

acc acc gct gaa ggt gca gat gaa atc gcc gag atg att cgc aat acg 307  
Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu Met Ile Arg Asn Thr  
55 60 65

tgg cca tca agc atc ttc cga aac gtt gag cta aag ggc gaa cca gct 355  
Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu Lys Gly Glu Pro Ala  
70 75 80 85

gat gaa gga gat ggt gtc act cgc gta cat ttc tcc tgc gaa tcc gca 403  
Asp Glu Gly Asp Gly Val Thr Arg Val His Phe Ser Cys Glu Ser Ala  
90 95 100

gac ttc aag tgc acg ggc att gtc cgc ctt cgt aat ggc aag gcg tgg 451  
Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg Asn Gly Lys Ala Trp  
105 110 115

acg cta ctc acc tca gct cgt gag ctc ctg gag cac cca gag ccc aag 499  
Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu His Pro Glu Pro Lys  
120 125 130

ggg cgc aac cgt gag atg ggc gtc gtc cat gga caa aat gag gac acc 547  
Gly Arg Asn Arg Glu Met Gly Val Val His Gly Gln Asn Glu Asp Thr

135	140	145	
cga aat tgg act gac Arg Asn Trp Thr Asp 150	cgc aag aat gat Arg Lys Asn Asp 155	cga caa gca gcg ttg ggt gtc Arg Gln Ala Ala Leu Gly Val 160	595
acc gag cag cca tac Thr Glu Gln Pro Tyr 170	acc ctc atc atc ggt Thr Leu Ile Ile Gly 175	ggt gga cag ggt ggc att Gly Gly Gly Gln Gly Ile 180	643
gcc ttg ggc gca cga ctc Ala Leu Gly Ala Arg 185	aag cga ctt ggt gta Leu Lys Arg Leu Gly 190	ccc gct cta atc att Pro Ala Leu Ile Ile 195	691
gat aaa gca tct cgc ccg Asp Lys Ala Ser Arg 200	ggc gac cag tgg cgt agc Gly Asp Gln Trp Arg 205	cgt tac cat tct Ser Arg Tyr His Ser 210	739
ctc tgc ctg cac gat Leu Cys Leu His Asp 215	cca gtt tgg tac gac Pro Val Trp Tyr Asp 220	cac ctg cct tac att cca His Leu Pro Tyr Ile Pro 225	787
ttc cca gat cat tgg Phe Pro Asp His Trp 230	cca gta ttt act cca Pro Val Phe Thr Pro 235	aag gac aag atg ggt gac Lys Asp Lys Met Gly Asp 240	835
tgg ctc gag cac tat Trp Leu Glu His Tyr 250	gtc ggc atc atg gat Val Gly Ile Met Asp 255	ttg gac tat tgg acc aac Leu Asp Tyr Trp Thr Asn 260	883
acc gag tgc ctg cgc Thr Glu Cys Leu Arg 265	gcc tca tac aat gag Ala Ser Tyr Asn Glu 270	gac acc aag cag tgg gat Asp Thr Lys Gln Trp Asp 275	931
gtg acg gtc aat cgt Val Thr Val Asn Arg 280	gat ggc gcg gag tcc Asp Gly Ala Glu Ser 285	acg ctc cac ccc acc caa Thr Leu His Pro Thr Gln 290	979
cta gtc atg gct act Leu Val Met Ala Thr 295	gga atg tcg ggc agc Met Ser Gly Ser Pro 300	ccg aac aaa cca act ttg Asn Lys Pro Thr Leu 305	1027
cct ggc cag gat aag Pro Gly Gln Asp Lys 310	ttc cag ggt gaa att Phe Gln Gly Glu Ile 315	cag cac tct tca gag cac Arg His Ser Ser Glu His 320	1075
ccc ggc ggc gat gtc Pro Gly Gly Asp Val 330	gat cgc gat aag aac Arg Asp Lys Asn Val 335	gtt gta gtt ctg ggc gct Val Val Val Leu Gly Ala 340	1123
aac aac tca gcc cac Asn Asn Ser Ala His 345	gac atc tgc gcg gat Asp Ile Cys Ala Asp 350	ctt tat tcc aat ggt gca Leu Tyr Ser Asn Gly Ala 355	1171
aag ccc gtg atg att Lys Pro Val Met Ile 360	cag cgc tcg tct aca Gln Arg Ser Ser Thr 365	cac atc gtg cgt tct gat His Ile Val Arg Ser Asp 370	1219
tcg ctg atg cgc gaa Ser Leu Met Arg Glu 375	gtc ttc ggg cct ctc Val Phe Gly Pro Leu 380	tat tct gag gat gcc gtt Tyr Ser Glu Asp Ala Val 385	1267

gaa gcc gga att gat acc gat act gcc gat ctc ctg ttt gcg tcg tgg 1315  
 Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu Leu Phe Ala Ser Trp  
 390 395 400 405  
  
 cca tat aag gtg ctg cca ggt gtg cag aag cag gct ttc gac aag atc 1363  
 Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln Ala Phe Asp Lys Ile  
 410 415 420  
  
 cgt gag gac gac aag gag ttc tac gac aag ctt gaa aat gct gga ttc 1411  
 Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu Glu Asn Ala Gly Phe  
 425 430 435  
  
 ttg ctt gat ttc ggc gat gac gat tcg ggg ctt ttc tta aag tac ctt 1459  
 Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu Phe Leu Lys Tyr Leu  
 440 445 450  
  
 cgc cgt ggc tct ggc tac tac atc gat gtc ggc gcc tct gaa ctg gtg 1507  
 Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly Ala Ser Glu Leu Val  
 455 460 465  
  
 gct gat gga aag att ccg gtg cgc tcc aat gtc agc att gaa gac gtc 1555  
 Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val Ser Ile Glu Asp Val  
 470 475 480 485  
  
 aag gaa aac tct gtg gtg ctc aca gat ggt act gag ctc cca gct gac 1603  
 Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr Glu Leu Pro Ala Asp  
 490 495 500  
  
 gtg att gtt cta gcg acc ggc tat gga aac atg aac aac tgg gtt gct 1651  
 Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met Asn Asn Trp Val Ala  
 505 510 515  
  
 cag ctg gtt gat cag gaa acc gct gac aag gtc ggc cca tgc tgg ggt 1699  
 Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val Gly Pro Cys Trp Gly  
 520 525 530  
  
 ctg ggc tct gaa acc acc aag gat cca ggc cca tgg gaa ggc gag ttg 1747  
 Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro Trp Glu Gly Glu Leu  
 535 540 545  
  
 cgc aat atg tgg aag ccc aca aac gtg gat tcg ctg tgg ttc cat ggt 1795  
 Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser Leu Trp Phe His Gly  
 550 555 560 565  
  
 ggc aac ctt cac cag tca cgc cat tac tca cgg tat ttg tcc atg cag 1843  
 Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg Tyr Leu Ser Met Gln  
 570 575 580  
  
 ttg aag gcg cgc tac gaa ggt atg aac act ccg gtg tac agc aag 1888  
 Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro Val Tyr Ser Lys  
 585 590 595  
  
 tagatacaaaa gaaaagggca tct 1911

&lt;210&gt; 420

&lt;211&gt; 596

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 420

Leu Pro Glu Gln Asp Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala  
 1 5 10 15  
 Phe Glu Lys Ala Thr Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala  
 20 25 30  
 Val Val Gln Leu Phe Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala  
 35 40 45  
 Phe Thr Trp Asn Leu Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu  
 50 55 60  
 Met Ile Arg Asn Thr Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu  
 65 70 75 80  
 Lys Gly Glu Pro Ala Asp Glu Gly Asp Gly Val Thr Arg Val His Phe  
 85 90 95  
 Ser Cys Glu Ser Ala Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg  
 100 105 110  
 Asn Gly Lys Ala Trp Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu  
 115 120 125  
 His Pro Glu Pro Lys Gly Arg Asn Arg Glu Met Gly Val Val His Gly  
 130 135 140  
 Gln Asn Glu Asp Thr Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln  
 145 150 155 160  
 Ala Ala Leu Gly Val Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly  
 165 170 175  
 Gly Gln Gly Gly Ile Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val  
 180 185 190  
 Pro Ala Leu Ile Ile Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg  
 195 200 205  
 Ser Arg Tyr His Ser Leu Cys Leu His Asp Pro Val Trp Tyr Asp His  
 210 215 220  
 Leu Pro Tyr Ile Pro Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys  
 225 230 235 240  
 Asp Lys Met Gly Asp Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu  
 245 250 255  
 Asp Tyr Trp Thr Asn Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp  
 260 265 270  
 Thr Lys Gln Trp Asp Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr  
 275 280 285  
 Leu His Pro Thr Gln Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro  
 290 295 300  
 Asn Lys Pro Thr Leu Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg  
 305 310 315 320

His Ser Ser Glu His Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val  
 325 330 335  
 Val Val Leu Gly Ala Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu  
 340 345 350  
 Tyr Ser Asn Gly Ala Lys Pro Val Met Ile Gln Arg Ser Ser Thr His  
 355 360 365  
 Ile Val Arg Ser Asp Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr  
 370 375 380  
 Ser Glu Asp Ala Val Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu  
 385 390 395 400  
 Leu Phe Ala Ser Trp Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln  
 405 410 415  
 Ala Phe Asp Lys Ile Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu  
 420 425 430  
 Glu Asn Ala Gly Phe Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu  
 435 440 445  
 Phe Leu Lys Tyr Leu Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly  
 450 455 460  
 Ala Ser Glu Leu Val Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val  
 465 470 475 480  
 Ser Ile Glu Asp Val Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr  
 485 490 495  
 Glu Leu Pro Ala Asp Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met  
 500 505 510  
 Asn Asn Trp Val Ala Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val  
 515 520 525  
 Gly Pro Cys Trp Gly Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro  
 530 535 540  
 Trp Glu Gly Glu Leu Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser  
 545 550 555 560  
 Leu Trp Phe His Gly Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg  
 565 570 575  
 Tyr Leu Ser Met Gln Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro  
 580 585 590  
 Val Tyr Ser Lys  
 595

&lt;210&gt; 421

&lt;211&gt; 367

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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<400> 421
gcccgaggact ttggcgtttc ggatcagcag ttcggttg attatggatt ctacgcgttt 60
gatcttccga tgcttcgcct catcgcttga ctcaactgtcg atg atg ttg atc gtt 115
Met Met Leu Ile Val
1 5

gct ttc ctg atc gca ctc gtt ggc cat tac ctc atg ggt ggc att cgc 163
Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu Met Gly Gly Ile Arg
10 15 20

gct gga aac cag atg acg ggc cag aag tcc ttt gta tcc cgt ggt gcg 211
Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe Val Ser Arg Gly Ala
25 30 35

cgc act cag ctt gcg gta act gct ggt ctg tgg atg ctt gtt aag gtc 259
Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp Met Leu Val Lys Val
40 45 50

gct ggc tac tgg ctg gat cgc tat gac ctg ctg act aag gaa aac tca 307
Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu Thr Lys Glu Asn Ser
55 60 65

acc ttc aca ggt gca agc tac acc gac atc aat gca cag ctg cca gcg 355
Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn Ala Gln Leu Pro Ala
70 75 80 85

aag atc atc ctg
Lys Ile Ile Leu 367

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<210> 422
<211> 89
<212> PRT
<213> Corynebacterium glutamicum
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<400> 422
Met Met Leu Ile Val Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu
  1             5             10             15
Met Gly Gly Ile Arg Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe
             20             25             30
Val Ser Arg Gly Ala Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp
             35             40             45
Met Leu Val Lys Val Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu
             50             55             60
Thr Lys Glu Asn Ser Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn
  65             70             75             80
Ala Gln Leu Pro Ala Lys Ile Ile Leu
             85

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<210>	424
<211>	154
<212>	PRT

<213> Corynebacterium glutamicum

<400> 424

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Val Thr Trp Ile Phe Ala Ile Ile Ala Leu Val Ile Leu Ile Ala Pro
 1           5           10           15
Met Ser Val Gly Phe Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp
          20           25           30
Phe Arg Gly Val Phe Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe
          35           40           45
Val Ile Phe Ala Leu Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr
          50           55           60
Phe Val Thr Lys Leu Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln
          65           70           75           80
Ser Pro Val Tyr Gln Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg
          85           90           95
Val Met Val Ile Ile Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile
          100          105          110
Gly Gln Arg Ser Trp Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp
          115          120          125
Phe Gly Val Ser Asp Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala
          130          135          140
Phe Asp Leu Pro Met Leu Arg Leu Ile Ala
          145          150

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<210> 425

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXA02684

<400> 425

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gcaggttcgt ccacagccgc cgggtgattgc aggggatggg gggaggcgtc gaaaagcaat 60
atcttttaag ccccggtggct gcctgggcac gatcgcgggc gtg ctt gct gtg ggc 115
                                   Val Leu Ala Val Gly
                                   1           5
ttg gtg ctt gtg ttt gtg gtg acg ctg tgg gcg gat tcg aag ctg aat 163
Leu Val Leu Val Phe Val Val Thr Leu Trp Ala Asp Ser Lys Leu Asn
          10           15           20
cgc gtg gat gcc acg cct gcg acg cag gtg gcg aac act gcc gga acg 211
Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala Asn Thr Ala Gly Thr
          25           30           35
aac tgg ctg ctg gta ggt tcg gat tcg cgg cag ggt tta agt gat gag 259
Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln Gly Leu Ser Asp Glu

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40	45	50	
gat att gag cgg cta ggt acc ggc ggc gat atc ggt gtg ggc cgt acg Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile Gly Val Gly Arg Thr 55 60 65			307
gac acg atc atg gtg ttg cat atg ccg cgt act ggc gag ccg acg ctg Asp Thr Ile Met Val Leu His Met Pro Arg Thr Gly Glu Pro Thr Leu 70 75 80 85			355
ttg tcg att ccg cgt gat tct tat gtc aat gtc cct ggc tgg ggc atg Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val Pro Gly Trp Gly Met 90 95 100			403
gat aag gca aac gcc gca ttt acc gtg ggt ggc ccg gaa ctg ctg acg Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly Pro Glu Leu Leu Thr 105 110 115			451
caa acc gtg gag gag gca act ggc ctg cga att gat cac tat gca gaa Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile Asp His Tyr Ala Glu 120 125 130			499
atc ggc atg ggt ggt ttg gcg aac atg gtt gat gcc gtg ggc ggc gtg Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp Ala Val Gly Gly Val 135 140 145			547
gaa atg tgt cct gct gag ccg atg tat gat ccg ctg gcg aac ctg gat Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro Leu Ala Asn Leu Asp 150 155 160 165			595
att cag gct ggt tgc cag gaa ttt gat ggg gca gcc gcg ctg ggt tat Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala Ala Ala Leu Gly Tyr 170 175 180			643
gtg cgc act cgt gcc aca gcc ctg ggt gat ctg gac cgg gtg gtg cgt Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu Asp Arg Val Val Arg 185 190 195			691
cag cgg gaa ttc ttc tcc gct ctg ctg agt aca gct acg tcc ccg ggc Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr Ala Thr Ser Pro Gly 200 205 210			739
acg ttg ctg aat ccg ttc cgc acc ttc ccg atg atc tcc aac gcg gtg Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met Ile Ser Asn Ala Val 215 220 225			787
gga aca ttc acc gtc ggc gag ggc gat cac gtg tgg cac ctg gcc cga Gly Thr Phe Thr Val Gly Glu Gly Asp His Val Trp His Leu Ala Arg 230 235 240 245			835
ttg gcg ctg gcg atg cgc gga gga atc gtg acg gag acc gtg ccg att Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr Glu Thr Val Pro Ile 250 255 260			883
gcc tca ttc gca gat tac gat gtg gga aat gtt gcg att tgg gac gaa Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val Ala Ile Trp Asp Glu 265 270 275			931
gct gga gcc gaa gca cta ttt agc tcc atg cgc taaaacccca ggtaatcggtt Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg 280 285			984

cac

987

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 426  
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 Asp Ser Lys Leu Asn Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala  
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 Asn Thr Ala Gly Thr Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln  
 35 40 45  
 Gly Leu Ser Asp Glu Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile  
 50 55 60  
 Gly Val Gly Arg Thr Asp Thr Ile Met Val Leu His Met Pro Arg Thr  
 65 70 75 80  
 Gly Glu Pro Thr Leu Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val  
 85 90 95  
 Pro Gly Trp Gly Met Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly  
 100 105 110  
 Pro Glu Leu Leu Thr Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile  
 115 120 125  
 Asp His Tyr Ala Glu Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp  
 130 135 140  
 Ala Val Gly Gly Val Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro  
 145 150 155 160  
 Leu Ala Asn Leu Asp Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala  
 165 170 175  
 Ala Ala Leu Gly Tyr Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu  
 180 185 190  
 Asp Arg Val Val Arg Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr  
 195 200 205  
 Ala Thr Ser Pro Gly Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met  
 210 215 220  
 Ile Ser Asn Ala Val Gly Thr Phe Thr Val Gly Glu Gly Asp His Val  
 225 230 235 240  
 Trp His Leu Ala Arg Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr  
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 Glu Thr Val Pro Ile Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val  
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 <223> RXN02391

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 Met Thr Gln Ser Asp  
 1 5  
 tta ccc gat gat gtt cag gaa ttg gtc act aag atc ttt gga ctg gca 163  
 Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys Ile Phe Gly Leu Ala  
 10 15 20  
 cgt gat ggg gga gca gaa tcc gca gca acc ctc ggt gca tat gtc gac 211  
 Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu Gly Ala Tyr Val Asp  
 25 30 35  
 aac ggc gtt gac gtt aac ctg tcc aac caa gat ggc aac act ttg ctc 259  
 Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp Gly Asn Thr Leu Leu  
 40 45 50  
 atg ctc gca gca tat gca gga cat gct gat gtc gtg cag gcg ttg att 307  
 Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val Val Gln Ala Leu Ile  
 55 60 65  
 gag cgt ggc gcc gat gtg gat cgc gtg aac aac cgc aat cag acg ccg 355  
 Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn Arg Asn Gln Thr Pro  
 70 75 80 85  
 ctg gcg ggc gcg atc ttt aag aag gaa gaa gcc gtc att gag gca ctg 403  
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 90 95 100  
 ctt gct ggt ggt gct gac cca tac gct gga act cca act gct gtt gat 451  
 Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr Pro Thr Ala Val Asp  
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 acc gcc aag atg ttt ggc cgc gag gat ctc gta gct cgc ttc gag tca 499  
 Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val Ala Arg Phe Glu Ser  
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<210> 428  
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 <213> Corynebacterium glutamicum



&lt;400&gt; 428

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 35 40 45

Gly Asn Thr Leu Leu Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val  
 50 55 60

Val Gln Ala Leu Ile Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn  
 65 70 75 80

Arg Asn Gln Thr Pro Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala  
 85 90 95

Val Ile Glu Ala Leu Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr  
 100 105 110

Pro Thr Ala Val Asp Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val  
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Ala Arg Phe Glu Ser  
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&lt;210&gt; 429

&lt;211&gt; 2826

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(2803)

&lt;223&gt; RXN02549

&lt;400&gt; 429

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gccgtaactg cagacgatgc cctgctcggt ggccctgagt atg gtt cac gcg aag 115  
 Met Val His Ala Lys  
 1 5

cag act aag aag cca ctt ccc cgt ttt ctt cac tcg gcg cat ttc tat 163  
 Gln Thr Lys Lys Pro Leu Pro Arg Phe Leu His Ser Ala His Phe Tyr  
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 Val Trp Ile Val Leu Gly Phe Val Val Phe Ala Gln Pro Tyr Gly Gln  
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gtt gct gcc gat act aaa cta gat ttg ctg ctc aac ccc gca gga ttt 259  
 Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu Asn Pro Ala Gly Phe  
 40 45 50

tta acc ggt gcg ctt cat gcg tgg act gac acg ttc acc ttg ggt cag 307  
 Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr Phe Thr Leu Gly Gln  
 55 60 65

ttg caa aac caa gct tat ggc tat ctg ttt ccc caa ggg ttt ttc ttc	355
Leu Gln Asn Gln Ala Tyr Gly Tyr Leu Phe Pro Gln Gly Phe Phe Phe	
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ctc ata act gat ttc ctc cct gac tgg att gcg cag cga ctg tgg tgg	403
Leu Ile Thr Asp Phe Leu Pro Asp Trp Ile Ala Gln Arg Leu Trp Trp	
90 95 100	
tgg ctt gtt ctt ggc ctg gga ttt tot gga ttc tac gca ctg gta gcc	451
Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe Tyr Ala Leu Val Ala	
105 110 115	
cgg ctg ggg att ggc aat cct gca ttc agg gtg atc gcc gcg ctg ctg	499
Arg Leu Gly Ile Gly Asn Pro Ala Phe Arg Val Ile Ala Ala Leu Leu	
120 125 130	
ttt gct ctg tcc ccg cgc acg ctc acc acc ctc act gca atc tcc tcc	547
Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu Thr Ala Ile Ser Ser	
135 140 145	
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Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val Cys Leu Pro Leu Leu	
150 155 160 165	
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Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu Ser Leu Leu Pro Ala	
170 175 180	
gca tgc atg ggt gca gtt aat gcc acc gcc acg atg gca gca ctc atc	691
Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr Met Ala Ala Leu Ile	
185 190 195	
ccg gca gcg ctg atc ttg ctg tat aga ggg ctc ttc tta agg ctg ctt	739
Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu Phe Leu Arg Leu Leu	
200 205 210	
ctg tgg gga atg ggc gtt ctc gct gtt aat tca tgg tgg atc gga cct	787
Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser Trp Trp Ile Gly Pro	
215 220 225	
ttg ttg gtg ctt ggc aaa tac gcc ccg ccc ttc acc gaa ttc atc gaa	835
Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe Thr Glu Phe Ile Glu	
230 235 240 245	
agt tcc tcc gtc acc act tcc tgg ctc aac cca gta gaa ata ctc cgc	883
Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro Val Glu Ile Leu Arg	
250 255 260	
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Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr Glu Arg Gln Ala Gly	
265 270 275	
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Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr Leu Ser Val Leu Val	
280 285 290	
gca gcc ctc ggc ttg atc ggc ctc acc ttg atg aaa cac cgt gga ctg	1027
Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met Lys His Arg Gly Leu	
295 300 305	

tgg gca ttc atg ctg gcc atc gga ctc ctc atc ctc ggc agc gcc cac Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile Leu Gly Ser Ala His 310 315 320 325	1075
cta acg gct gtt caa gaa ttc ctc gac ggc cca ggc gca gca ctt cga Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro Gly Ala Ala Leu Arg 330 335 340	1123
aac atc cac aaa ttt gat cta tta gtc cgc atg ccg ttg atg gtg ggc Asn Ile His Lys Phe Asp Leu Leu Val Arg Met Pro Leu Met Val Gly 345 350 355	1171
gtt gcc gca ttg ggg tcg cat atc agt ctg ccc ttg ctt ggg acg act Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro Leu Leu Gly Thr Thr 360 365 370	1219
gca ttg acc agc gga caa ggc aaa cac cac acc atc ccg ctg cct ctc Ala Leu Thr Ser Gly Gln Gly Lys His His Thr Ile Pro Leu Pro Leu 375 380 385	1267
caa aaa cgc caa gcc gca gga ctc ctc gtg gtg atc atc gct gtc ggt Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val Ile Ile Ala Val Gly 390 395 400 405	1315
gct ctt gct ccc gca tgg tcg gca cgg ctg cta cct cag gga acg tgg Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu Pro Gln Gly Thr Trp 410 415 420	1363
gat gaa gtg cct gac tac tgg tac gaa gcc aca gaa ttc ctc aac caa Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr Glu Phe Leu Asn Gln 425 430 435	1411
aac gcc aca ggc acc cgc acg ttg att tgg cct agc tcg ccg ttt gcc Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro Ser Ser Pro Phe Ala 440 445 450	1459
cgc cag gac tgg gga tgg act cgg gat gaa cca gct caa cca ctt ctt Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro Ala Gln Pro Leu Leu 455 460 465	1507
gat gtt ccg tgg gct gtc cgc gat gcc att cct ttg gtt ccc ccg gag Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro Leu Val Pro Pro Glu 470 475 480 485	1555
gcg att cgc gga tta gat ggt ctc gac gac cta ggc act cta ggc acc Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu Gly Thr Leu Gly Thr 490 495 500	1603
ggt cta aac gac gag gct tta aaa cgt cta ggc atc ggc gca gta ctg Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly Ile Gly Ala Val Leu 505 510 515	1651
gtg agg cat gat ctg gaa gcc gac cca gat att gag gtg gat ctg cct Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile Glu Val Asp Leu Pro 520 525 530	1699
ggg gaa aag cac act ttt ggc tcc caa ggc caa gta gac gtc tac ctc Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln Val Asp Val Tyr Leu 535 540 545	1747
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Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser Gly Thr Ser Lys Gln 550 555 560 565	
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atc aac ggc tat tcc ccg agg act ttg gtg agt gag aat gcc cag atc Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser Glu Asn Ala Gln Ile 585 590 595	1891
gtc acc gat acc cct cag cta gtc ggc aca aat tac ggc gat ggc acc Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn Tyr Gly Asp Gly Thr 600 605 610	1939
agt tcc gca gca ttg gcc agc ctt gat gag act gag gtg aaa aac cgc Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr Glu Val Lys Asn Arg 615 620 625	1987
atc gtg gat tat cct tcc gcg ggg cca atg acg cag gtg gtg cag gaa Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr Gln Val Val Gln Glu 630 635 640 645	2035
ggc tcc atc acg gcg tct tcg tct ggt tcc gat gcc act tct ttc ggc Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp Ala Thr Ser Phe Gly 650 655 660	2083
ggc gcg gat cct gat cgt tcc ctt aat tca ctt ctt gat cat cgt tac Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu Leu Asp His Arg Tyr 665 670 675	2131
aac acc gcc tgg tac ccg aca cct ggc gat acg tct ccg tgg ctc gaa Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr Ser Pro Trp Leu Glu 680 685 690	2179
gtc tcc ggt acc ggc acc aca tta tcg atc tcc ccc cgc agc acc gtc Val Ser Gly Thr Gly Thr Leu Ser Ile Ser Pro Arg Ser Thr Val 695 700 705	2227
acc gcc acc atc acc tcc ggc gat tcc gtg atg gtc cgc gag ttc gaa Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met Val Arg Glu Phe Glu 710 715 720 725	2275
aaa ggc cgc acc acc aca gtt acg ttg gcg gag cct gaa gct cgc att Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu Pro Glu Ala Arg Ile 730 735 740	2323
gaa ttc gat ggt ttc gta gga att tcc gag ctg tcc cta gag ggt ctc Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu Ser Leu Glu Gly Leu 745 750 755	2371
agc cgc acc atc act gtg ccg gag acc tct cct gac gtg cag caa ttc Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro Asp Val Gln Gln Phe 760 765 770	2419
gtt ttc caa cgc ctc aca gtg ccc acc tcg ttc ctc gac cgc act ttc Val Phe Gln Arg Leu Thr Val Pro Thr Ser Phe Leu Asp Arg Thr Phe 775 780 785	2467
aca gtc ccc cgc cac atg tcc gtc acc gtg gag gcc caa tcc tgc gtc Thr Val Pro Arg His Met Ser Val Thr Val Glu Ala Gln Ser Cys Val	2515

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Thr Leu Glu Leu Asp Gly Asp Arg Ile Asp Cys Gly Pro Ser Asn Ser				
810		815	820	
ccc ccg gaa ccc aca cgc tgc gca ccc aat cgg aat ggg tca ccc tca				2611
Pro Pro Glu Pro Thr Arg Cys Ala Pro Asn Arg Asn Gly Ser Pro Ser				
825		830	835	
ccg aat ccg ctc cgc tcg ccg ctg ttc agc cag caa caa aca tcg agg				2659
Pro Asn Pro Leu Arg Ser Pro Leu Phe Ser Gln Gln Gln Thr Ser Arg				
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Gln His Pro Pro Thr Ala Cys Ser Ser Pro Arg Ala Leu Ser Ile Gln				
855		860	865	
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Val Pro Ala Arg Leu Ser Thr Pro Pro Pro Phe Pro Gln Ser Asn Ser				
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Thr Pro Pro Pro Lys Val Ser Ser Ser Pro Arg Thr Pro Pro Ala Ser				
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&lt;210&gt; 430

&lt;211&gt; 901

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

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Gln	Pro	Tyr	Gly	Gln	Val	Ala	Ala	Asp	Thr	Lys	Leu	Asp	Leu	Leu	Leu
		35					40					45			

Asn	Pro	Ala	Gly	Phe	Leu	Thr	Gly	Ala	Leu	His	Ala	Trp	Thr	Asp	Thr
		50				55					60				

Phe	Thr	Leu	Gly	Gln	Leu	Gln	Asn	Gln	Ala	Tyr	Gly	Tyr	Leu	Phe	Pro
	65				70				75						80

Gln	Gly	Phe	Phe	Phe	Leu	Ile	Thr	Asp	Phe	Leu	Pro	Asp	Trp	Ile	Ala
				85					90					95	

Gln	Arg	Leu	Trp	Trp	Trp	Leu	Val	Leu	Gly	Leu	Gly	Phe	Ser	Gly	Phe
		100						105					110		

Tyr	Ala	Leu	Val	Ala	Arg	Leu	Gly	Ile	Gly	Asn	Pro	Ala	Phe	Arg	Val
		115					120					125			

Ile	Ala	Ala	Leu	Leu	Phe	Ala	Leu	Ser	Pro	Arg	Thr	Leu	Thr	Thr	Leu
	130					135					140				

Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val  
 145 150 155 160  
 Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu  
 165 170 175  
 Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr  
 180 185 190  
 Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu  
 195 200 205  
 Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser  
 210 215 220  
 Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe  
 225 230 235 240  
 Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro  
 245 250 255  
 Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr  
 260 265 270  
 Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr  
 275 280 285  
 Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met  
 290 295 300  
 Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile  
 305 310 315 320  
 Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro  
 325 330 335  
 Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val Arg Met  
 340 345 350  
 Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro  
 355 360 365  
 Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His His Thr  
 370 375 380  
 Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val  
 385 390 395 400  
 Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu  
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 Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr  
 420 425 430  
 Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro  
 435 440 445  
 Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro  
 450 455 460

Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro  
 465 470 475 480  
 Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu  
 485 490 495  
 Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly  
 500 505 510  
 Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile  
 515 520 525  
 Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln  
 530 535 540  
 Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser  
 545 550 555 560  
 Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu  
 565 570 575  
 Ser Leu Leu Asp Thr Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser  
 580 585 590  
 Glu Asn Ala Gln Ile Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn  
 595 600 605  
 Tyr Gly Asp Gly Thr Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr  
 610 615 620  
 Glu Val Lys Asn Arg Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr  
 625 630 635 640  
 Gln Val Val Gln Glu Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp  
 645 650 655  
 Ala Thr Ser Phe Gly Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu  
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 Leu Asp His Arg Tyr Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr  
 675 680 685  
 Ser Pro Trp Leu Glu Val Ser Gly Thr Gly Thr Thr Leu Ser Ile Ser  
 690 695 700  
 Pro Arg Ser Thr Val Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met  
 705 710 715 720  
 Val Arg Glu Phe Glu Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu  
 725 730 735  
 Pro Glu Ala Arg Ile Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu  
 740 745 750  
 Ser Leu Glu Gly Leu Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro  
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				Val	Leu	Gly	Thr	Asn								
				1								5				
gtg	ttt	ggt	gcg	ctc	gca	gta	atg	ctg	ttt	gtg	cgc	ttc	ctc	att	ccg	163
Val	Phe	Gly	Ala	Leu	Ala	Val	Met	Leu	Phe	Val	Arg	Phe	Leu	Ile	Pro	
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cag	cca	gat	gct	tca	aat	ttc	aac	gct	gag	atc	tcg	tat	ctg	cca	gct	211
Gln	Pro	Asp	Ala	Ser	Asn	Phe	Asn	Ala	Glu	Ile	Ser	Tyr	Leu	Pro	Ala	
			25					30					35			
gtt	ggt	ttc	gca	tac	ctg	gcg	ttc	gcc	att	gtc	gcg	ggc	atg	ctg	gtg	259
Val	Gly	Phe	Ala	Tyr	Leu	Ala	Phe	Ala	Ile	Val	Ala	Gly	Met	Leu	Val	
			40					45					50			
aca	ttt	ttg	atg	ttc	cgc	ccg	gtg	ctt	gat	tgg	cag	cga	agc	cct	gaa	307
Thr	Phe	Leu	Met	Phe	Arg	Pro	Val	Leu	Asp	Trp	Gln	Arg	Ser	Pro	Glu	
			55					60					65			
gat	cat	gac	cga	aat	atg	gtg	cgc	aac	ttg	gtt	atg	cgc	atc	ccc	atc	355
Asp	His	Asp	Arg	Asn	Met	Val	Arg	Asn	Leu	Val	Met	Arg	Ile	Pro	Ile	
			70					75					80	85		



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Tyr Gln Ala Ile Leu Cys Ala Val Val Trp Leu Ile Gly Ile Ala Ile	
90 95 100	
gca acg ttg att tgc gcc agt gtg tct acc agt ttg gcg ctg gtc gtg	451
Ala Thr Leu Ile Ser Ala Ser Val Ser Thr Ser Leu Ala Leu Val Val	
105 110 115	
gcg ttt tcc acg ttg atg gct gcc gca atc gtc gtg ctg ctc acc tac	499
Ala Phe Ser Thr Leu Met Ala Ala Ala Ile Val Val Leu Leu Thr Tyr	
120 125 130	
ctt gag gct gag cgt ttg gtg cgt ccg gtt gct gcg tct gcc ctg gcg	547
Leu Glu Ala Glu Arg Leu Val Arg Pro Val Ala Ala Ser Ala Leu Ala	
135 140 145	
cgt cga ttt gag gat tcc acg ctg gaa cca cct gtg agc cag cgc ttg	595
Arg Arg Phe Glu Asp Ser Thr Leu Glu Pro Pro Val Ser Gln Arg Leu	
150 155 160 165	
cgt atg acg tgg ttg ctg acg ttg ggc att cca gtg atg gga att ctg	643
Arg Met Thr Trp Leu Leu Thr Leu Gly Ile Pro Val Met Gly Ile Leu	
170 175 180	
ctg ctt att tgg ggc tac tgc cag ggc att ttc ggc tct gat gcc tcc	691
Leu Leu Ile Trp Gly Tyr Ser Gln Gly Ile Phe Gly Ser Asp Ala Ser	
185 190 195	
gga att atg cct gcc atc gca gcg ctc gcg ttt gca tgc ttg gtc acg	739
Gly Ile Met Pro Ala Ile Ala Ala Leu Ala Phe Ala Ser Leu Val Thr	
200 205 210	
ggt tac ctg ggc aac cgg ctt gtg gtg tcc tct gtg gtg gat ccg att	787
Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser Val Val Asp Pro Ile	
215 220 225	
cgg gaa ctt cag gag gcc atc aac agg gtt cgt cgt ggt gaa aac gat	835
Arg Glu Leu Gln Glu Ala Ile Asn Arg Val Arg Arg Gly Glu Asn Asp	
230 235 240 245	
gtg cag gtt gat att tat gat ggc tct gag atc ggt gtg ctt cag gct	883
Val Gln Val Asp Ile Tyr Asp Gly Ser Glu Ile Gly Val Leu Gln Ala	
250 255 260	
ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc cgt	931
Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val Arg	
265 270 275	
gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg ctg	979
Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala Leu	
280 285 290	
gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg ttg	1027
Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val Leu	
295 300 305	
ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act cct	1075
Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr Pro	
310 315 320 325	
gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg gag	1123

Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val Glu  
 330 335 340  
 gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac gcg 1171  
 Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp Ala  
 345 350 355  
 gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc ggt 1219  
 Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr Gly  
 360 365 370  
 cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat ctc 1267  
 His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp Leu  
 375 380 385  
 cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct ggt 1315  
 Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala Gly  
 390 395 400 405  
 cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac gcg 1363  
 His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp Ala  
 410 415 420  
 gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca ggc 1411  
 Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro Gly  
 425 430 435  
 cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg gag 1459  
 Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala Glu  
 440 445 450  
 cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt agc 1507  
 Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg Ser  
 455 460 465  
 cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat agg 1555  
 Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp Arg  
 470 475 480 485  
 tcc taatacgtt ttcgacgcaa aaa 1581  
 Ser

&lt;210&gt; 432

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 432

Val Leu Gly Thr Asn Val Phe Gly Ala Leu Ala Val Met Leu Phe Val  
 1 5 10 15

Arg Phe Leu Ile Pro Gln Pro Asp Ala Ser Asn Phe Asn Ala Glu Ile  
 20 25 30

Ser Tyr Leu Pro Ala Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val  
 35 40 45

Ala Gly Met Leu Val Thr Phe Leu Met Phe Arg Pro Val Leu Asp Trp  
 50 55 60

Gln Arg Ser Pro Glu Asp His Asp Arg Asn Met Val Arg Asn Leu Val  
 65 70 75 80  
 Met Arg Ile Pro Ile Tyr Gln Ala Ile Leu Cys Ala Val Val Trp Leu  
 85 90 95  
 Ile Gly Ile Ala Ile Ala Thr Leu Ile Ser Ala Ser Val Ser Thr Ser  
 100 105 110  
 Leu Ala Leu Val Val Ala Phe Ser Thr Leu Met Ala Ala Ala Ile Val  
 115 120 125  
 Val Leu Leu Thr Tyr Leu Glu Ala Glu Arg Leu Val Arg Pro Val Ala  
 130 135 140  
 Ala Ser Ala Leu Ala Arg Arg Phe Glu Asp Ser Thr Leu Glu Pro Pro  
 145 150 155 160  
 Val Ser Gln Arg Leu Arg Met Thr Trp Leu Leu Thr Leu Gly Ile Pro  
 165 170 175  
 Val Met Gly Ile Leu Leu Leu Ile Trp Gly Tyr Ser Gln Gly Ile Phe  
 180 185 190  
 Gly Ser Asp Ala Ser Gly Ile Met Pro Ala Ile Ala Ala Leu Ala Phe  
 195 200 205  
 Ala Ser Leu Val Thr Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser  
 210 215 220  
 Val Val Asp Pro Ile Arg Glu Leu Gln Glu Ala Ile Asn Arg Val Arg  
 225 230 235 240  
 Arg Gly Glu Asn Asp Val Gln Val Asp Ile Tyr Asp Gly Ser Glu Ile  
 245 250 255  
 Gly Val Leu Gln Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu  
 260 265 270  
 Arg Gln Arg Val Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val  
 275 280 285  
 Ala Lys Arg Ala Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg  
 290 295 300  
 Lys Val Ala Val Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala  
 305 310 315 320  
 Val Asn His Thr Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe  
 325 330 335  
 Glu His Val Val Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys  
 340 345 350  
 Phe Gln Gly Asp Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu  
 355 360 365  
 Ser Asp Ala Thr Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala  
 370 375 380

Glu Leu Lys Asp Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly  
 385 390 395 400  
 His Val Val Ala Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr  
 405 410 415  
 Val Ile Gly Asp Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala  
 420 425 430  
 Lys Thr Thr Pro Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu  
 435 440 445  
 Ala Asn Glu Ala Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu  
 450 455 460  
 Leu Arg Gly Arg Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro  
 465 470 475 480  
 Thr Leu Ala Asp Arg Ser  
 485

<210> 433  
 <211> 1008  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(985)  
 <223> RXS01425

<400> 433  
 agtccctatt aatcccaagg agtttcgact cacagtgtc aatttcattt attggccaat 60  
 ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat 115  
 Val Leu Ser Pro Asp  
 1 5  
 tcc gga att acc tgg gcc ttg tgc atc atg ttc ttg acc ttc acc gtg 163  
 Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val  
 10 15 20  
 cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc 211  
 Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg  
 25 30 35  
 aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac 259  
 Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr  
 40 45 50  
 aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa 307  
 Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys  
 55 60 65  
 gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag 355  
 Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln  
 70 75 80 85  
 atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc 403  
 Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg

90	95	100	
acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala 105 110 115			451
aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu 120 125 130			499
cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro 135 140 145			547
gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn 150 155 160 165			595
atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr 170 175 180			643
cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala 185 190 195			691
gcc ggc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met 200 205 210			739
caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu 215 220 225			787
ttc acc ggc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser 230 235 240 245			835
aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met 250 255 260			883
gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg 265 270 275			931
act acc gct cca aag cct ggc gtg aag cca gaa aac ccc aag aag cgt Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg 280 285 290			979
aag aag taaaacttca ctaaaaaccg cca Lys Lys 295			1008

&lt;210&gt; 434

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe  
 1 5 10 15  
 Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr  
 20 25 30  
 Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala  
 35 40 45  
 Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr  
 50 55 60  
 Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu  
 65 70 75 80  
 Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu  
 85 90 95  
 Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr  
 100 105 110  
 Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu  
 115 120 125  
 Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser  
 130 135 140  
 Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp  
 145 150 155 160  
 Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile  
 165 170 175  
 Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln  
 180 185 190  
 Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln  
 195 200 205  
 Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met  
 210 215 220  
 Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu  
 225 230 235 240  
 Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr  
 245 250 255  
 Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys  
 260 265 270  
 Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu  
 275 280 285  
 Asn Pro Lys Lys Arg Lys Lys  
 290 295

&lt;210&gt; 435

&lt;211&gt; 1856

&lt;212&gt; DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1833)

<223> RXS01658

<400> 435

gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga	48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg	
1 5 10 15	
aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta	96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val	
20 25 30	
gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca	144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro	
35 40 45	
aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt	192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val	
50 55 60	
tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat	240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp	
65 70 75 80	
gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac	288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr	
85 90 95	
acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat	336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp	
100 105 110	
gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga	384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly	
115 120 125	
cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt	432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly	
130 135 140	
gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac	480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr	
145 150 155 160	
acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt	528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg	
165 170 175	
gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat	576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp	
180 185 190	
cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc	624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser	
195 200 205	
cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac	672

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr	
210 215 220	
cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc	720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr	
225 230 235 240	
acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg	768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala	
245 250 255	
act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca	816
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr	
260 265 270	
gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg	864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala	
275 280 285	
tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt	912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val	
290 295 300	
ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg	960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser	
305 310 315 320	
gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg	1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu	
325 330 335	
ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct	1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser	
340 345 350	
gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca	1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro	
355 360 365	
act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg	1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val	
370 375 380	
gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc	1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr	
385 390 395 400	
ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg	1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala	
405 410 415	
tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct	1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro	
420 425 430	
acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg	1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met	
435 440 445	
tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac	1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn	



450                      455                      460  
 gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag 1440  
 Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu  
 465                      470                      475                      480  
 atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg 1488  
 Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser  
                     485                      490                      495  
 gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt 1536  
 Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val  
                     500                      505                      510  
 ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat 1584  
 Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp  
                     515                      520                      525  
 ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg 1632  
 Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr  
                     530                      535                      540  
 cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa 1680  
 Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu  
 545                      550                      555                      560  
 acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac 1728  
 Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn  
                     565                      570                      575  
 gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag 1776  
 Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu  
                     580                      585                      590  
 tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag 1824  
 Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln  
                     595                      600                      605  
 tcc gca cag tagcgtttga gtaaacagcc cga 1856  
 Ser Ala Gln  
 610

&lt;210&gt; 436

&lt;211&gt; 611

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 436

Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg  
 1                      5                      10                      15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val  
 20                      25                      30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro  
 35                      40                      45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val  
 50                      55                      60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp  
 65 70 75 80  
 Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr  
 85 90 95  
 Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp  
 100 105 110  
 Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly  
 115 120 125  
 Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly  
 130 135 140  
 Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr  
 145 150 155 160  
 Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg  
 165 170 175  
 Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp  
 180 185 190  
 Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser  
 195 200 205  
 Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr  
 210 215 220  
 Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr  
 225 230 235 240  
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala  
 245 250 255  
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr  
 260 265 270  
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala  
 275 280 285  
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val  
 290 295 300  
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser  
 305 310 315 320  
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu  
 325 330 335  
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser  
 340 345 350  
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro  
 355 360 365  
 Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val  
 370 375 380  
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr

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<210> 437
<211> 867
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(844)  
<223> RXS01677
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<400> 437
gtcgccatag ttgagtttta ttcatggctt ttagctaggc gacttttagtt gagggctttt 60
agttgagggc ttcccagcag ggatggttaa ggagaattca gtg aac caa cag agt 115
Val Asn Gln Gln Ser
1 5

```

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc 163  
 Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu  
                   10                                  15                                  20

atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc 211  
 Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala  
                   25                                  30                                  35

gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act 259  
 Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr  
                   40                                  45                                  50

gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc 307  
 Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser  
                   55                                  60                                  65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat 355  
 Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp  
                   70                                  75                                  80                                  85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt 403  
 Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys  
                                   90                                  95                                  100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa 451  
 Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu  
                                   105                                  110                                  115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa 499  
 Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu  
                   120                                  125                                  130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac 547  
 Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp  
                   135                                  140                                  145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc 595  
 Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro  
                   150                                  155                                  160                                  165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac 643  
 Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp  
                                   170                                  175                                  180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa 691  
 Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu  
                                   185                                  190                                  195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc 739  
 Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly  
                   200                                  205                                  210

gcc tac tcc acc cca gct ttc ctc cta ggt gcc cag cca atc atg gcc 787  
 Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly  
                   215                                  220                                  225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca 835  
 Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala  
                   230                                  235                                  240                                  245

gcg aaa gaa taaaccgtgg atgtcggcct agt  
Ala Lys Glu

867

<210> 438  
<211> 248  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 438  
Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile  
1 5 10 15  
Ile Ala Val Leu Leu Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn  
20 25 30  
Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser  
35 40 45  
Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp  
50 55 60  
Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala  
65 70 75 80  
Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr  
85 90 95  
Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met  
100 105 110  
Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val  
115 120 125  
Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala  
130 135 140  
Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala  
145 150 155 160  
Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile  
165 170 175  
Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp  
180 185 190  
Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu  
195 200 205  
Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly  
210 215 220  
Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe  
225 230 235 240  
Glu Gln Ala Leu Ala Ala Lys Glu  
245

<210> 439

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<220>  
<221> CDS  
<222> (101)..(1072)  
<223> RXS02932
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<400> 439															
cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gccaccact															60
agcagcacca tttcagtttt aactttcttg gagttttcta															115
Val Ser Lys Thr Glu															1
gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att															163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile															10 15 20
ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg															211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro															25 30 35
ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg															259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met															40 45 50
ggg ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca															307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro															55 60 65
ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc															355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe															70 75 80 85
ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc															403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala															90 95 100
gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat															451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn															105 110 115
gtg att gcg ttt ctc gcc cgaggga gat gtc gcg cta tcg gtc acc atg															499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met															120 125 130
acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg															547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met															135 140 145
ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg															595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala															150 155 160 165
tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt															643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val															170 175 180
ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt															691

Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu  
 185 190 195  
 cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc 739  
 Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val  
 200 205 210  
 gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt 787  
 Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val  
 215 220 225  
 gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc 835  
 Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr  
 230 235 240 245  
 ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att 883  
 Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile  
 250 255 260  
 gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga 931  
 Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg  
 265 270 275  
 ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc 979  
 Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val  
 280 285 290  
 cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct 1027  
 His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro  
 295 300 305  
 ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc 1072  
 Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser  
 310 315 320  
 taacttattt gctgcccggtt aga 1095

&lt;210&gt; 440

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala  
 1 5 10 15  
 Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro  
 20 25 30  
 Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile  
 35 40 45  
 Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met  
 50 55 60  
 Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe  
 65 70 75 80  
 Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu  
 85 90 95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly  
                   100                                  105                                  110  
 Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala  
                   115                                  120                                  125  
 Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met  
                   130                                  135                                  140  
 Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp  
 145                                  150                                  155                                  160  
 Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val  
                                   165                                  170                                  175  
 Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys  
                   180                                  185                                  190  
 Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val  
                   195                                  200                                  205  
 Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly  
                   210                                  215                                  220  
 Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val  
 225                                  230                                  235                                  240  
 Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn  
                   245                                  250                                  255  
 Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser  
                   260                                  265                                  270  
 Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala  
                   275                                  280                                  285  
 Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu  
                   290                                  295                                  300  
 Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val  
 305                                  310                                  315                                  320  
 Ala Val Ser Ser

<210> 441  
 <211> 844  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(844)  
 <223> FRXA02402

<400> 441  
 cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gcccaccact 60  
 agcacgacca tttagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa 115



											Val 1	Ser	Lys	Thr	Glu 5	
gaa Glu	ggc Gly	cgt Arg	tca Ser	gcg Ala 10	gcc Ala	ata Ile	att Ile	att Ile	tac Tyr 15	gcg Ala	ttt Phe	cca Pro	act Thr	ttc Phe 20	att Ile	163
ctg Leu	ctg Leu	ggc Gly	gcg Ala 25	atc Ile	att Ile	gcg Ala	ttt Phe	atc Ile 30	ttc Phe	ccg Pro	gaa Glu	cca Pro	ttc Phe 35	att Ile	ccg Pro	211
ctg Leu	aca Thr	aac Asn 40	tac Tyr	att Ile	aat Asn	atc Ile	ttc Phe 45	ctc Leu	acg Thr	atc Ile	atc Ile	atg Met 50	ttc Phe	acc Thr	atg Met	259
ggt Gly	ttg Leu 55	acc Thr	ttg Leu	acg Thr	gtg Val	ccc Pro 60	gat Asp	ttt Phe	cag Gln	atg Met	gtg Val 65	ctt Leu	aaa Lys	cgt Arg	cca Pro	307
ctg Leu 70	cct Pro	atc Ile	ttg Leu	atc Ile	ggt Gly 75	gta Val	gta Val	gcg Ala	cag Gln	ttt Phe 80	gtc Val	atc Ile	atg Met	cca Pro	ttc Phe 85	355
ctg Leu	gcg Ala	atc Ile	gtg Val	gtt Val 90	gcg Ala	aaa Lys	atg Met	ttc Phe	aac Asn 95	ctc Leu	aac Asn	cca Pro	gca Ala	ctc Leu 100	gcc Ala	403
gtt Val	ggc Gly	ctt Leu	ctc Leu 105	atg Met	ctg Leu	gga Gly	tcc Ser	gtt Val 110	ccg Pro	ggg Gly	ggc Gly	acc Thr	tcc Ser 115	tcc Ser	aat Asn	451
gtg Val	att Ile	gcg Ala 120	ttt Phe	ctc Leu	gcc Ala	cga Arg	gga Gly 125	gat Asp	gtc Val	gcg Ala	cta Leu	tcg Ser 130	gtc Val	acc Thr	atg Met	499
acc Thr	tct Ser	gtg Val	tcc Ser	acc Thr	att Ile	gtt Val 140	tcc Ser	cca Pro	atc Ile	atg Met	acg Thr 145	cct Pro	ttc Phe	ctc Leu	atg Met	547
ctc Leu 150	atg Met	ctg Leu	gca Ala	ggt Gly 155	act Thr	gaa Glu	acc Thr	gcc Ala	gtc Val	gat Asp 160	ggg Gly	gga Gly	ggc Gly	atg Met	gcg Ala 165	595
tgg Trp	act Thr	ttg Leu	gta Val	caa Gln 170	aca Thr	gtg Val	ctg Leu	ctg Leu	cct Pro	gtg Val	atc Ile	atc Ile	ggc Gly	cta Leu 180	gtt Val	643
ctg Leu	cgt Arg	gtc Val	ttc Phe 185	ttg Leu	aac Asn	aag Lys	tgg Trp	atc Ile 190	gac Asp	aag Lys	att Ile	ttg Leu	ccg Pro 195	atc Ile	ctt Leu	691
cct Pro	tat Tyr	ctc Leu 200	tcc Ser	atc Ile	ctc Leu	ggt Gly	atc Ile 205	ggt Gly	ggc Gly	gtg Val	gtg Val	ttc Phe 210	ggc Gly	gca Ala	gtc Val	739
gca Ala	gcc Ala 215	aac Asn	gcg Ala	gaa Glu	cga Arg	ctc Leu 220	gtg Val	tct Ser	gtc Val	gga Gly	ctc Leu 225	atc Ile	gtg Val	ttc Phe	gtt Val	787
gca Ala	gtt Val	atc Ile	gtg Val	cac His	aac Asn	gta Val	ctt Leu	gga Gly	tac Tyr	gtt Val	gtg Val	gga Gly	tac Tyr	ctc Leu	acc Thr	835

230

235

240

245

ggc cgt gta  
Gly Arg Val

844

&lt;210&gt; 442

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala  
1 5 10 15

Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro  
20 25 30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile  
35 40 45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met  
50 55 60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe  
65 70 75 80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu  
85 90 95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly  
100 105 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala  
115 120 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met  
130 135 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp  
145 150 155 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val  
165 170 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys  
180 185 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val  
195 200 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly  
210 215 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val  
225 230 235 240

Val Gly Tyr Leu Thr Gly Arg Val  
245



gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu 185 190 195	691
acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn 200 205 210	739
gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val 215 220 225	787
atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly 230 235 240 245	835
cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp 250 255 260	883
acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr 265 270 275	931
cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile 280 285 290	979
tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg 295 300 305	1027
aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu 310 315 320 325	1075
cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn 330 335 340	1123
gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr 345 350 355	1171
caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg 360 365 370	1219
gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn 375 380 385	1267
gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln 390 395 400 405	1315
gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu 410 415 420	1363

gac tgatgttgatg gaccaatcga gat  
Asp

1389

&lt;210&gt; 444

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp  
1 5 10 15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp  
20 25 30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala  
35 40 45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile  
50 55 60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp  
65 70 75 80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys  
85 90 95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln  
100 105 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg  
115 120 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu  
130 135 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val  
145 150 155 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu  
165 170 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile  
180 185 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg  
195 200 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu  
210 215 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser  
225 230 235 240

Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val  
245 250 255

Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile  
260 265 270

Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu  
 275 280 285

Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe  
 290 295 300

Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp  
 305 310 315 320

Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg  
 325 330 335

Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn  
 340 345 350

Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg  
 355 360 365

Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile  
 370 375 380

Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys  
 385 390 395 400

Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg  
 405 410 415

Glu Pro Ser Gln Glu Asp  
 420

<210> 445  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 445  
 ggaaacagta tgaccatg

18

<210> 446  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 446  
 gtaaaacgac ggccagt

18